```
C.Accession: 004388

R:Bult. C.J.: White O. Colsen of T. Zhon E. Firlischmann, R.D., Sutton, G.G., Riake, R.Bult. C.J.: White O. Colsen of T. Zhon E. Firlischmann, R.D., Sutton, G.G., Riake, R. Reich, O. I. Overbook, R.: Kirkness, E.F.; Weinstonk, K.G., Merrick, T.M., Glodek, A. rson, J.D., Sulta, F.W., Harra, M.C., Cutton, M.D., Scheits, K.M., Hurst, M.A. Science 273, 1058 1073, 1946

A:Authors: Kaine R.F.: Berodowsky M.: Klenk, H.P.: Fraser, C.M.: Smith, H.O.: Woese, J. A.; Authors: G. M.: Science archive sequence of the methanogenic archaeve, Methanogenic januaschii A:Reiterence number: A64300: MUID:96337999: pMID:8688087
A:Authors: Hunter, J.L.: Jenkins, J.: Johnson-Hopson, C.: Khan, S.: Khaykin, E.: Kim, C. C.A.; Li, J.H.: Li, Y.: Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.: Marziali, Rizzo, M.: Rechey, T.: Rowley, D.: Sakano, H.
A:Authors: Salyherta, S.L.: Schwartz, J.R.: Shinn, P.: Southwick, A.M.: Sun, H.: Tallon, Ker. M.: Wu. D.: Yu. G.: Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141: MOID:21016719: PMID:11130712
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A:Title: Deciphering the bickey of Mysokasterium tuberculosis from the complete genome
A:Reference number: A70500; MOID:98295987; PMID:9634230
A:Accession: R70888
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R;Cole, S.T.; Brosch R: Parkhill J; Garnier, T; Churcher, C; Harris, L; Gordon, S; Connor, R: Povies, P: Devlin, K; Feltwell, T: Gentles, S: Hamlin, N; Holroyd, S; Connor, R: Squares, S; Bajandream, M.A.: Rogers J; Rutter, S; Seeger, K; Skelton, S; Squares, S; Nature 393, 537-544, 1998

Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                          Charcession: A95595
R-Theologis A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.: Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Australia preliminary, nucleic acid sequence not shown, translation not shown Armolecula type. CRA
Auresidues: 1-322 <BML>
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Cisperies: Methanococcus jannaschii
Cipathe (18:Sepeluus #sequence_revision 18:Sepeluus #rext_charge 21-Jul-2000
                                                                                                                                                                                                                                                                      Chin. C.W.: Chung. M.K.: Conn. L.: ansen. N.F.: Hughes. B.: Huizar, L. Nature 408. 816-820, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein T1M13 2 (imported) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mai 2201 #sequence_revision 02-Mai-2001 #text_change 31-Mar-2001
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A, Fittle: Snapshot of a large dynamic replicon in a halophilic Archaeon: megaplasmid of A:Reference number: Z16408: MUID:9964795; PMID:9847077
A:Accession: T08277
A:Status: translated from GB/EMB. (TIBJ A. Molecule type. DNA A. Residues: 1:379 < NGN-A, Residues: 1:379 <
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Genome Res. 8, 1131-1141, 1998
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A:Status: preliminary
A:Melecule type: DNA
A:Residues: 1-354 <STO>
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C;Genetics: ......
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Search completed: April 8, 2003, Job time: 26,0833 secs
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Fred. No. 1.4e+02:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     score 25; DB 2; Length 379;
Pred. No. 1.5e+02;
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Assene, pls:
C:Superfamily: mouse l-acylolycerol-3-ph
C:Keywords acyltransferase: coencyme A
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A:Accression. $44281
A:Molecule type: mFNA
A:Resslues: 1-227 \SPE\
A:Cross-reterences: EMBL:X77575; NID:g482918; PID:g1345528
                                                                                                                                                                                                 A:Starus: preliminary
A:Molevule type: DNA
A:Residues 1-237 (ARN)
A:Cross-reterences: GR-AE001550; GB:AE001439; NID:q4155872; PIDN:AAD05852.1; PID:q415588
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A:FILLE: Complete genome Sequence of an aerobin byper-thorrophillic Cucharshauth. Actupy
A:Reterence number: A72450; MUID:99310339; PMID:10382966
A:Accession: G72484
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R:Speulman, E.: Salamini, F.
submitted to the EMBL Data Library. February 1994
                                                                                                                                             C:Genetics:
                                                                                                                                                                               A:Experimental source: strain J99
                                                                                                                                                                                                                                                                                                                         A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A:Reference number. A71800: MUID:POIDASET; PMID 9923632 A:Accession: B71827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #fext_change of oct-2000 C:Accession: B71827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable 1-acylolycerol 3-phosphate 0-acyltransferase (EC 2.3.1.51) - Helicobacter pylon SiSpecies: Helicobacter pylon
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A:Residues: 1-235 <KAW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aypothetini protein APE2519 - Aeropyrum pernix (strain Ki)
C.Species: Aeropyrum pernix
C.Dare: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_chauge 20-Aug-1999
                                                                                :Superfamily: mouse l-acylolycerol-3-phosphate O-acyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :Accession: 372484
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   4. .th Libell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 100.0%; Score 25; DB
Local Similarity 100.0%; Pred. No. 93;
hes 5; Conservative o Mismatoles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 LESYI 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LESYT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e Similarity
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      100.00
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Scott 25.
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C:Reywords: acyltransforase; cochayme A
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R:Tomb J.F.: White, O.: Kerlavane, A.R.: Clayton, R.A.: Sutton, G.G.: Fleischmann, R:Tomb J.F.: White, O.: Kerlavane, A.R.: Clayton, B. Kiajak, H.G. Sisske, A.: M. Fefriesen, G. Tottus, B. Ficherlan, C.: Waith
                                                                                                                                                                                                                                                                                                                                                                                                          A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; A;Title: Massive gene decay in the leprosy bacillus. A;Reference number: A86909; MUII:::1128932; FMID::11234002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C:Pate: 10 Apri201 #sequence_redision 20 Apri200 #text_change 20 Apri200
C:Accession: G86920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Authors: Wallin, E.: Hayes, W.S.) Borodovsky, M.: Karpk, P.D.: Smith, H.D.: Fraser. A:Title: The complete genome sephone of the dastric pathogen Halicohacter pylori. A:Reterence number: A64520; MUID: 97394467; PMID: 9252185
A:Accession: D64688
                                                                                                                                                                                                                       A:Gene: ML0095
                                                                                                                                                                                                                                                                      A/Cross-references: GB:AL450380: NID:q13092477; PIDN:CAC29603.1; G3PDB:GN00147
                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-302 <STOS
                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                             A:Accession: G86920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 409,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eam, M.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R., Cole, S.T., Eiglmeier, K., Parkhill, J., James, K.D.; Thomson, N.R.; Wheeler. R.; Davies, R.M.; Devlin, K.; Davioy, S.; Feltwell, T.; Frascr A.; Hamlin, N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable integral membrane protein (imported)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G86920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Cross-references: GR:AF000636:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-240 <TOM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable 1-acylglycerol-3-phosphate 0-acyltransferase (BC 2.3.1.51) - Helicobacter py
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .vioss-references: GB:AF000636: GB:AE000511: NID:q2314517: PIDN:AAD08393.1: Fii-q231:
;Superfamily: mouse 1-acylglyc::51:3 phosphate 0-acyltransferase
:Romwords: hoult-reference
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.Date. 09-Aug-1997 #sequence_re.iskon 09-Aug-1997 #text_change 06 Oct-2000
                                                                                                          Matches
                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                 Genetics:
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210 LESYT 214
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                                                                                                                                 Lucaa
                                                   1 LESYT 5
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J. Kelley, J.M.: Cotton, M.D.: Weidman, J.M.: Fujii, C.: Bowman, C.: Watthey.
38, 539-547, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1007-1011, 2001
                                                                                                                                 Similarity
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                                                                                                          Conservative
                                                                                                                                 100.0%
130.JE
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                                                                                                                              Score 25: DB 2; Fred. No. 1.2e+3
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Pred. No. 95;
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                                                                                                          Mismatches
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                                                                                                                           1.20102;
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                                                                                                                                                              Length 302:
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C:Species: Mycobacterium tuberculosis C:Sate: 17 Julily90 #sequence\_te..s.on 17-Julily98 #text\_change 22-nct-1999

hypothetical protein Rv3806c - Mycobacterium tuberculosis (Strain H37RV)

RESULT 12

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5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arrett, R.A.; Ragan, M.A.: Sensen, C.W.; Van der cost, submitted to GenBank. April 2001
a:Description: Sulfolobus solfatarious complete genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conserved byperbetical protein (imported) . Sulfolobus solfatarious cospecies; Sulfolobus solfatarious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Status preliminary
A:Molecule type DNA
A:Residons: 1-133 <KUR>
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C:Superfunkly: conserved hypothetical protein MJ1552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Cross-reteledeces. GB.AED00641; NID:q10813694; PIDN-AAK40852 1: GSPDB-GN00155
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                                                                                                                                                                                                                                                                                                                                                                                              A:Experimental source: cultivar Columbia
R:Lin. X.: Kaul. S.: Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.: Mottat, K.S.; Cronin, L.A.: Shen, M.: VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.: Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                          A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A:Reference number: A84420: MUID:20083487; PMID:10617197 A:Accession: G84655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; kesidues: 1-190 <ROU>
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                                                                                A:Map position: 2
2:Supertamily: Arabidopsis thaliana hypothetical protein T13J8.30
                                                                                                                                         A;Gene: T19L18.15; At2q26040
                                                                                                                                                                                            A;Cross-references: GB:AE002093; NID:q3413709, FIDN:AAC31232.1; GSPDB:GN00139
                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-190 <STO>
                                                                                                                                                                                                                                                                                     A:Status: preliminary
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:Arcession: E90199
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Accession: E90199
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Best Local S
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Best Local Similarity
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I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder,
, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
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hes 5; Conservative (
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S: Conserv
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  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lis. X., Ketchum, K.A.; Crosby, M.L., Brandon P.C.
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     Score 25:
Pred. No.
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                                   DB 2:
                                   Length 190
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RESNE, D.: Singh, K.K.: Confabrator, E., Errander, Y.: Allard, G.: Awayez, M. Jong, T.: Jeffries, A.C.: Kozera C.J.: Modina, N.: Peng, X.: Thi-Ngoc, H.P.: arrett, R.A.: Ragan, M.A.: Senson, C.W.: Van der Oost, J. submitted to GenBark, April 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Reference number: A99139
A:Accession: E90187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C:Date: 24-May 2001 #sequence_:regision 24-May-2001 #iext_charge 15 Jun 2001 C:Accession: E90187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           haml protein [imported] - Sult Tobus solfatarious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: $500432
C;Supertamily: Methanococcus jaunaschii conserved hypothetical protein MJ0226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Description: Sulfolobus solf darious complete genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Molecule type:
A:Residues: 1:19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-Tixing Cyanobacterin A;Reference number: AB1807; MUIC:21595285; PMID:11759840
A;Accession: AH2547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Kaneko, T.; Nakamura, Y.; Wolk, C.F.; Kuritz, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CiSpecies: Nostoc sp. arrain PCC 7/20 is a synonym of Anabaena sp. strain PCC cipate: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_charge 30-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AP003602: PIDN:BAB77310.1; PID:q17134752; GSPDB:GNe0181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Status: preliminary
A:Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                   A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                         A:Gene: alr7667
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Residuos: 1-215 KMR>
c:Species: Hordeum vulgare (bailey)
c:Date: 13-Jan 1995 #sequence_revision 13-Jan-1995 #text_change 24-Mar-1999
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                                              ES43 protein - barley
                                                                   $44281
                                                                                            RESULT
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100.0%; Pred. No. 75;
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Fred. No. 85;
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Database :
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Listing first 45 summaries
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25
1 LESYT 5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

No.   Score   Match Length CB   15   160.0   39   2   365.295   100.0   138   2   25   100.0   140   2   70.2619   25   100.0   140   2   70.2619   25   100.0   216   2   2   244.281   25   100.0   216   2   2   244.281   25   100.0   227   2   244.281   25   100.0   235   2   267.2484   25   100.0   235   2   267.2484   25   100.0   236   2   2   2   2   2   2   2   2   2	primosomal protein	D8173	753	190.0	5.3	54
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# ALIGNMENTS

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                                                                                     Amino acid sequence
Protein of WT-MCP-
    Human chemokine hM
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Novel hyman diagno	ARGINAING4	ij	n,		. n	<u>ب</u> را
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Arabidopsis thalla	AAC07699		354		25	40
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Human prostate can	AAY48330	t-	282	100.0	25	ين اگر
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Polymorphic varian	ABG35168	†	109	00.	25	25
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Human MC proprotei	AAW42072	, T	109		25	2.4
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Wild type monocyte	AAY07237	24	99		25	21
Wild type monocyte	AAYOT 222	1	30	ЭG.	t J	t) co
C-C chemokine, McF	AAY05300	Ö	55	00.	25	19
Human chemotactic	ABB11828	t	95	100.0	53 53	18
Chimeric chemokine	AAGERRES	1 =1	4	100.0	io in	)
Mouse/human hybrid	AAGTRAGA	~	4	100 0	r3 - n	- T
Chimeric chemokine	AAG68358	اد. ند	77		25	15
Mouse/human hybrid	3588 DWV	1.	77	100.0	C)	14
Human MCP2 tragmen	AHRHHHÜB	A.,	77	90.	l Un	<u>, т</u>
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Human monocyte che	AAG68353	۸. غ	7.5	100.0	25	11

### ALTONMENTS

RESULT 1 AAY49695 ID AAY4 design legical dependently edisodes HIV-1: envelope protein: qpl20; t.x; t.c. t. av t.s.c., ital sell stems for viral intention; neuronal sell death; encyphalispathy: neuropathy inemory loss; dementia depression; psychosis; opportunistic infection; neurotoxicity; inflammatory neurological disease; multiple sclerosis; tropical spastic paraparesis; Alzheimer's disease. PIV 1 apring induced year hal cell death inhibiting peptide #1. WPI- 1999-633635/54 W09951254-A1. AAY49695 Standard: poptible 5 Synthetic. 19. TAN-2000 (first entr.) Pert C, (ADIM-) ADVANCED IMMUNIT INC 06-APR-1998; 06-APR-1999; 14-0CT-1999 Ruif M; 41 MUS-0080M 14 99WO-US07' Ã

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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogeni polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by Flathes the discrete include SATH, syndrome (synchia, actor, pustulosis, hypertosis and osteomyelitis), uncitis and endophthalmitis
                                                                                                                                                       Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                           N-PSDB; AAS59578
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbcnt assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU56783 standard; Protein; 50 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 11; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New peptides useful for labibiring human inmuno-deficiency virus type (HIV-1) gp120 induced neuronal cell death -
                                                                                                   Example 1; SEQ ID No 17978; 1069pp; English
                                                                                                                                                                                                                                                              L'maisonneuve J, Zhang
                                                                                                                                                                                                                                                                                   Skeiky YAW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   induced neuronal cell death. Pharmaceutical compositions containing the
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5: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and AAY49696 represent peptides which inhibit HIV-1 gp120
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Pred. No. 7.8e+05;
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acces proteins. These antibodies can be used to downraymate expression and activity of P. acces polypeptides and therefore treat P. acces infections. The antibodies may also be used as diagnostic agents for determining P. acces presence for example, by enzyme linked immunoscribert assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 he series is also involved in infections of bear joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with some vulgaris. A method for detecting the presence or absence of P. acres in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention
                                                                                                                                                                                                                                                                            30 20N 2000 20000 5-0608408
03-APG-2000 20000S-063246
21-SEP-2000 20000S-023467
27-SEP-2000 20000S-0236654
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                                                                                                                                                                                                                                                                                                                                                            04-FEB-2000; 200005-018632
                                                                                                                                                                                                                                                                                                                                                                                                                                                        W0200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               microarray; Alzheimer's discase; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; brain expressed exon: gene expression analysis: probe
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                                                                                                                                                                                                                                                                 04-00T-2000; 2000GH-0024263
                                                                                                                                                                                                                                                                                                                                            25-MAY-2000; 200008-0207456
                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001; 2001WO-US0C667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human brain expressed single exon probe encoded protein SE2 ID
                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAM1 😤 INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 LESYT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LESYT 5
                                                                                                                                                                                                     Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                      Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 25: DB 22;
Pred. No. 1.1e+02;
                                                                                                                                                                                                      Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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probes which are derived from genomic sequences expressed in the human brain. They can be used to an asure gene expression to brain cell samples, which may eachle the diamons and improved frommost of normous system diseases such as Altheimon's disease multiple solerosis, wohizophrenia,

The present invention provides a number of single exon nucleic acid Example 4; SEQ ID NO:  $36\pm69$ ; 650pp + Sequence Listing; English WPI; 2001-483446/52

Single exem nucleic acts (dobes for analyzing gene expression in

human

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RESULT 4
AAY07234
ID AAY0
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                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                  are useful as medicaments, for diagnosis and/or treatment of diseases which require antagonistic activity of a chemokine e.g. inflammatory diseases. HIV infection fumours, and antiogenesis and hematopoicsis related diseases, including auto-immune diseases, athorosclerosis, pulmonary diseases and skin disorders.
                                                                                                                                                                                                                          This sequence regressets a truncated Cof chemoking motoryte observable protein 2 (MCF2) containing amino acids 6.76 of the mature protein. The invention relates the generation of amino-terminal truncated CoC chemokines, having chemokine antagonistic activity. The new chemokines
                                                                                                                                                                                                                                                                                                                                                    New amino-terminally truncated C·C chemokines have antagonistic activity for treatment of immune, inflammatory and infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regulated on activation normal T-cell expressed and secreted; RANTES; truncation: antagonist medicaments diagnosis; inflammation; infertion; tumour; audiovenessis, hematicpolessis, antoimmune disease atherosclerosis; pulmonary disease; skin disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                         Claim 4; Fig 1; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    WPI: 1999 LC7108/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ISTE ) ARS APPLIED RES SYSTEMS HOLDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07 - APR - 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wild type; C-C chemokine; monocyte chemotactic protein 2; MCP2; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-301-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY07234 standard; protein; 71 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP906954-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Truncated monocyte chemotactic protein 2 (6-76)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                             tocal Similarity
hes 5: Conserv
20 LESYT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 LESYT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LESYT 5
                            1 LESYT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                              Struyt S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97EP-0116863.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97EP-0116863.
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                                                                         100.0%;
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Pred. No. 1.5e+02;
                                                                         Score 25; DB 20;
Pred: No. 1 Ke+02;
                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                      Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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AAR70804
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                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                             This sequence represents a translated C C chemokine monocyte chemotactic protein Z (MCPZ) contained amino acids 6-76 of the mature protein. The invention relates the generation of aminoctornical conversed CC chemokines, having chemokine antagonistic activity. The new chemokines are useful as medicaments, for diagnostic activity. The new chemokines are useful as medicaments, for diagnosts and/or treatment of diseases which require antagonistic activity of a chemokine e.g. inflammatory diseases, HTV infection, fundous, and analogenesis, and hematopolesis—related diseases, including auto-immune diseases, atheroscierosis,
Chemoattractant; MCP-2; h-paranase; heparin; heparan sulfate;
                              Chemoattractant MCP-2.
                                                                                            AAR70804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New amino-terminally trun-sted (**) chemokines have autagonistic activity for treatment of immune, inflammatory and infectious
                                                            29-AUG-1995
                                                                                                                       AAR70804 standard; Protein;
                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                     pulmonary diseases and skin disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Fig 1: 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wp1: 1949-206774/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-DEC-1997;
29-SEP-1497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulated on activation resmal T-cell expressed and secreted: RANTES: truncation; antagonist: Redicaments; diagnosis; inflammation; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wild type; C-C chemokine: monocyte chemotactic protein 2: MCP2; HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Truncated monocyte chemotactic protein 2 (6-76).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUL-1999 (first entr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY07238 standard; protein: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EF905241-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pulmonary disease: skin disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumour; anglogenesis; hematopolesis; autoimmune disease; atherosclerosis;
                                                                                                                                                                                                 20 LESYT 24
                                                                                                                                                                                                                            1 LESYT 5
                                                                                                                                                                                                                                                            Conservative
                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97EP-0116863.
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                                                                                                                                                                                                                                                                            100.
                                                                                                                                                                                                                                                            <u>.</u>
                                                                                                                                                                                                                                                                        Ered. No. 1.6e+02;
                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                       Length 71;
                                                                                                                                                                                                                                                            Indels
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McDonald JR, Coggins PJ;

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AAY69031
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      purified heparanases, prepared under reducing conditions and activated with transdiutaminase, are given in AR70786-804. Most are prepared by reverse transcription of mPNA from activated human leukocytes, then clocking of the CDNA into pVL1392 baculowirus vector, and expression in Sf9 cells in the presence of reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Screening for cpds, with anti-heparanase activity - by detecting inhibition of heparin or heparan sulphate degradation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UPJO ) UPJOHN CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arthritis: restenosis; cancer; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 13; Page 53: 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          potentially useful for treating arthritis, restenosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI: 1995-082239/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hooywert AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUL-1993;
13-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                AAY69.31 standard; protein; 76 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glutathione and dithiothreitol.
                                                                                      03-FEB-2000
                                                                                                                                                                                                     secondary tissue damage; central nervous system injury; MCP-2; CNS inflammatory disease; neurodegenerative disorder; heart disease; inflammatory bowel disease;
                                                                                                                                                                                                                                            Chemokine receptor; ligand; inflammatory response; immune effector cell;
                                                                                                                                                               inflammatory thyroid disease; thyroiditis; cytokine-regulated cancer
                                                                                                                                                                                                                                                                    Amino acid sequence of chemokine receptor ligand MCP-2.
                                                                                                                                                                                                                                                                                              30-MAY-2000 (first entry)
            (SEPR-) OSPREY PHARM LID
                                                              21-JUL-1999;
                                                                                                                                         Homo sapiens.
                                                                                                                                                                                           inflammatory
                                     22-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                  23 LESYT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LESYT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ledbetter SR;
                                                                                                                                                                              joint disease; inflammatory kidney; renal disease lung disease; inflammatory nasal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93US-0136117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        998660m-Suse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94WO-US08207
                                       98nS-0120523
                                                               99WO-CA00659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 25; DB 16;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Best Local Similarity
Trackes 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a chemokine receptor liquid. The present induid can be incorporated into the conjugates of the invention. The specification describes a combigate binds to a chemokine receptor rigand. The conjugate binds to a chemokine receptor resulting in internalisation of the targeted agent in cells bearing the receptor. The conjugates are used for formulating a medicament or for treating disorders associated with inflammatory responses resulting from activation, proliferation and migration of immune effector cells. The disorders or disease states comprise secondary tissue damage such as central nervous system (CMS) injury. CNS inflammatory diseases, inflammatory bowel diseases, inflammatory boint diseases, inflammatory inflammatory board diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A new therapeutic agent compulsing a conjugate for treating secondary tissue damage and other disease conditions like Alzheimer's disease stroke, Parkinson's disease and atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WFI, 2000-182542/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 60; 204pg. English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammatory bowel diseases, inflammatory joint diseases, inflammatory hing diseases, inflammatory hing diseases, inflammatory hand diseases, inflammatory hand disease such as thyroiditis, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytokine-regulated cancers
                                                                                                                                                                                                                                                                                                                                                            PANTES: neuroprotective: antiallergic: actinitlammatory anti-HIV: chemokine mutant; catton: site; multiple sclerosis; HIV infection:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA021099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAO21099 standard: Protein.
                                                                                                                                                                                                                                                                                                                                                                                                                   protein of WT-MCP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUL-2002 (first entr)
A mutant of the human CC chemokine RANTES with two mutations in the callionic site of the 40 \% loop is used for treatment of multiple sclerosis and/or demyelhating diseases -
                                                                     WPI; 2002-340073/37
                                                                                                       Proudfoot A, Wells TNC, Kosco-Vilbois
                                                                                                                                     (ISTF ) ARS APPLIED RES SYSTEMS HOLDING
                                                                                                                                                                         04-OCT-2000; 2000EP-0121mp5
                                                                                                                                                                                                           03.OCT-2001; 2001WO-EP11420
                                                                                                                                                                                                                                             11-APR-2002
                                                                                                                                                                                                                                                                               WO200228419-A2
                                                                                                                                                                                                                                                                                                                                             inflammatory disease; demyelinating disease; allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 LESYT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LESYT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soure 25.
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21:
1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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Examples: Page 46: 46pp; English

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AAO21109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                      The invention relates to a truncated and mutated human PANTES (a CC chemokine mutant), comprising the amino sequence of 91 amino acids as given in the specification. The CC chemokine mutant RANTES, with two mutations in the cationic site is useful for the preparation of a pharmaceutical composition used in treating multiple sclerosis or other demyelinating diseases. The mutant with single mutations at cationic sites is used for the treatment of HIV infection and/or other allergic or inflammatory diseases. This sequence represents an example of a CC inflammatory diseases. This sequence represents an example of a CC
                                                                                                                                                                                                                              A mutant of the human CC chemokine RANTES with two mutations in the cationic site of the 40's loop is used for treatment of multiple sclerosis and/or demyelinating diseases -
                                                                                                                                                                                              Disclosure; Fig 1; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chemokine mutant), comprising the amino sequence of 91 amino acids as given in the specification. The CC chemokine mutant RANTES, with two mutations in the cationic site is useful for the preparation of a pharmaceutical composition used in treating multiple sclerosis or other demyelinating diseases. The mutant with single mutations at cationic sites is used for the treatment of HIV infection and/or other allergic or inflammatory diseases. This sequence represents an example of a wild-type
             chemokine protein
                                                                                                                                                                                                                                                                                                                                                   Proudfoot A, Wells INC,
                                                                                                                                                                                                                                                                                                                                                                                 (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV
                                                                                                                                                                                                                                                                                                                                                                                                                     04-001-2000; 2000EP-0121665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W0200228419-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RANTES: neuroprotective; antiallergic; antiinflammatory; anti-HIV; human; chemokine mutant; cationic site; multiple sclerosis; HIV infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA021109 standard; Protein; 76 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammatory disease; demyelinating disease; allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MCP-2 chemokine protein containing 40's loop and cationic site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUL-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a truncated and mutated human RANTES (a CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chemokine protein used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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46..49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Cationic_site
         ises. This sequence represents an example of a CC containing a 40^{\circ}\mathrm{S} loop and cattering site of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                 Kosco-Vilbois M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Pred. No. 1.7e+02;
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                   here the antigen present is the composition is a tumour associated antigon. The use of APC clambdaxins provides an accelerated immune response in a bast following administration of antigen, a more effective temponse to administratification, if exposure to, very small quantities of
                                                                                             infectious pathmy-nic agents (bacteria, virus, etc.,) prior to expected or possible exposure, for treating cancers, melanomas, tung and breast cancers, renal cell carcinomas etc.
                                                                                                                                                                              separately. Synthetic (missage) or naturally occurring chemokines may be used. The polypeptides of the invention are used to induce an immune response by recruiting AFGs to areas of antigen contact. The compositions
                                                                                                                                                                                                                                         This title and antimized at activity. The compositions of the invention can contain one or more antigens (or antigen containing polynucleotides) and may be administered in the same mixture as the APC chemptaxin or
                                                                                                                                                                                                                                                                                                     subject, in the manufacture of a medicament, where the APC-chemotaxin is a chemokine polypeptide or its variant, or a polynucleotide encoding the chemokine polypeptide or its variant. The invention has antitumour,
an antigen (e.g., toxin () pathogen) due to increased autigen uptake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of a composition containing an antigen presenting cell-chemotaxin which is a chemokine polymeptide or its variant or a polymucleotide encoding the protein, for inducing immune response to an antigen in a
                                                                                                                                                                                                                                                                                                                                                                 describes the use of a composition containing an antigen presenting cell (APC) -chamotaxin for inducing an immune response to an untigen in a
                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of a human chemokine polypeptide designated hMCP-2, used in the compactions of the invention. The specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Fig 2; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-034405/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schall TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHEM-) CHEMOCENTRYX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-APR-2000; 2000US-1988 (4P
12-APR-2001; 2001US-0834814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W0200180882-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chemokine; antitumour; cytostatic; antimicrobial; toxin; pathogenic agent; cancer. melanoma; thyroid carcinoma; renal cell carcinoma; tumour-associated antigen; human; hMCP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG78390 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigen presenting cell; APC; chemotaxin; immune response; antigen;
                                                                                                                                                             the invention are useful for providing protection from foreign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 LESYT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 0%; Score 25; 100 0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                           The specification
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RESULT 11
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                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human: mouse; monocyte chemotactic protein 2; hMCP2, MCP2; mCl0: chimeric chemokine; immune response; cytostatic; antimicrobial; immunostimulant; vaccine; cancer; breast cancer; lung cancer; carcinoma, melanoma; tumour; hyprikine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human monocyte chemotactic protein 2 (MCP2) amino acid sequence
                                                                                              composition containing an antigen-presenting cell chemotaxin (APC-chemotaxin), where the APC-chemotaxin is a chemokine polypeptide of its variant, or a polypnocleoride encoding the chemokine polypeptide of its variant. The APC-chemotaxin has cytostatic antimorphial and immunestimulari activities, and can be used for inducing or enhancing an immune response. The method can be used for inducing or enhancing an immune response. The providing protection from exogenous foreign infectious pathogenic or for providing protection from exogenous foreign infectious pathogenic displaying symptoms of exposure. The method may be used to treat cancers e.g. breast cancers, lung cancer, carcinomas, melanomas, and tumours. The present sequence represents a human monocyte chemotactic protein 2 present sequence represents a human monocyte chemotactic chemokines).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Inducing an immune response to an antigen to confer non-specific protection while the body is generating the adaptive response, comprises administering a composition containing an antigen-presenting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-APR-2001; 2001W0-US12162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHEM-) CHEMOCENTRYX INC
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tes 5: Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                         cell chemotaxin
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                                                                                                                                                                                                                                                                                                                                  The present invention describes a method for inducing an immune response to an antiqen in a subject. The method comprises administering a
                                                                    Sequence
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 Local Similarity
hes 5; Conserv
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ilarity 100.0%: Pred. No. 1.7e+02;
conservative 0; Mismatches of
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 Conservative
                    100.0%; Score 25; DB 23; 100.0%; Pred. No. 1.7e+02;
       0;
       Mismatches
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                                          Length 76;
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1 LESYT 5 ||||| 26 LESYT 30

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RESULT 12
AAB15786
ID AAB15
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Best Local Similarity 10: 0%; Scote 25; DB 21; 1499th 77; Matches 5; Conservative 0: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monoryre chemoattractant protein-1; inflammation; atherosclerosis; HIV: monoryre chemoattractant protein-1; inflammation; atherosclerosis; HIV: AIDS; stroke; psoriasis; autoimmune disease; hypertension; ender-xaemia; basophil-mediated disease impocardial infarction; acute ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human chemokine MCP-2 SEQ 1D NC: 17
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17-MAR-1999;
01-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macrophage recruitment; chamokine derivative; MCP-1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rheumatoid arthritis; contraception
                                                                                                                         The present invention concerns the identification of a number of chemokines which can be used to produce derivatives, appulsts and antagonists which are then useful in disease treatment. The chemokines antagonists which are then useful in disease treatment. The chemokines antagonists which are then useful in disease treatment. The chemokines can be used to treat diseases such as these can be used to treat diseases such as autommune diseases, atheroscierosis, osteoporosis, HIV inherition and autommune diseases, atheroscierosis, osteoporosis, HIV inherition and AIRS, psoriasis, inflammatory diseases, hypertension, hasophil-mediated diseases, endotoxaemia, myocardial infarction, acute incharmia and diseases, endotoxaemia, myocardial infarction, acute incharma and rehumatorid arthritis, and can be used to prevent strokes and as remained the coding sequences for the chemokines can be used in gene therapy for the same diseases, as well as in the production of gene therapy for the same diseases, as well as in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUL-2000.
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                                                                                                                                                                                                                                                                                                                                                                                              New peptide 3, amide and heterocyclic compounds and saccharide conjugates used for inhibiting chemokine induced activity and for treating e.g. stroke, vaccular diseases, autoimmune diseases and tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grainger DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAA74886.
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                                                                                                                                                                                                                                                                                                                                         Example 1; Page 134; 387pp; English.
                                                                           Sequence
                                                                                                                animal models.
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                                                                                  77 AA;
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99US-02711/2.
99US-04524(6.
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AAG78395
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                                    RESULT 14
                                                                                                                                                                                                                                                                     The invention relates to polynucleutides encoding muting julner his or chuman ectaxin polypeptides. The ectaxin polypucleotides are useful for modulating essimphil chemotraxis, for increasing eximphil chemotractic events, and for improving prognosis with tumours in parious They are also useful for treating inflammation and tumourlegenesis, and for reducing inflammatic near damage caused by ecsimphils, for educing inflammatic reactions, eosimophilic pnounchia and allergic diseases, inflammatory bowel diseases, atopic dematitis, urticatia, vascultis, parasitic infections and eosimophil cardiac diseases. The cotaxin polynucleotides are also useful for modulating histamine release by modulating ectaxin activity or expression during anaphylaxis, curticaria and allergic reactions. They are useful for detecting and monitoring eosimophil mediating conditions, and in anti-cancer gene therapy. The present sequence represents a human monocyte chemicative converter (Murby) frazment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB80903
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                                                                                                                                                                                           Query Match
AAG78395 standard; protein; 77 AA
                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                protein (MCP)2 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disciosure; Fig 3B; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New DNA encoding murine, guinea pig or human eotaxin polypeptides, useful for treating inflammation and tumorigenesis and in anticancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI - 2002-565447,760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Luster AD, Leder P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy; antianaphylactic.
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                                                                                                                                                          Local Similarity
nes 5; Conserv
                                                                                        25 LESYT 30
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                                                                                                                                                        Conservative
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                                                                                                                                                                       100.0%; Score 25; DB 23; 100.0%; Pred. No. 1.7e+02;
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antigen containing polynorlectides) and may be administered in the same mixture as the APC-chemotaxin or separately. Synthetic (minetic) or naturally occurring chemotaxin or separately. Synthetic (minetic) or naturally occurring chemotaxin or separately. Synthetic (minetic) or naturally occurring chemotaxin or separately. Synthetic (minetic) or naturally occurring chemotaxins may be used. The polypeptides of the invention are useful for providing protection from foreign infectious pathogenic agents (bacteria, virus, etc.) prior to expected or possible exposure; for treating cancers, melanomas, thyroid carcinomas, lung and breast cancers, renal cell carcinomas etc. here the antigen present in the composition is a tumour-associated antigen. The use of APC-chemotaxins provides an accelerated immune response in a host following administration of or exposure to very small quantities of au antigen (e.g., toxin or pathogen) due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of a chimeric chemokine polypeptide (hybridkine) derived from bundan chemokine hMGP 2 (AAC78396) and murine chemokine mMDC (AAC78392) used in the compositions of the invention. The specification describes the use of a composition containing an antigen presenting cell (APC)-chemotaxin for inducing an immune response to an antigen presenting cell (APC)-chemotaxin for inducing an immune response to an antigen presenting cell (APC)-chemotaxin for inducing an immune response to an antigen to a subject to manufacture of a subject to 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antigen in a subject, in the manufacture of a medicament, where the APC-chamataxin is a chemakine polypeptide or its variant, or a polypurcleotide encoding the chemokine polypeptide or its variant. The invention has antitumour cytostatic and antimicrobial activity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of a composition containing an antigen presenting cell chemotaxin which is a chemokine polymeptide or its variant or a polymerleotide encoding the protein, for inducing immune response to an autique in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            compositions of the invention can contain one or more antigens (or
                                                                                                     increased antigen uptake by APCs, and more effective anti-tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 5, Fig 2, 60pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antigen presenting cell; APC; chemotaxin; immune response; antigen; chemokine, antitumour; cytostatic; antimicrobial; toxir; pathogenic agent: cancer melanoma: thyroid carcinoma; hybridkine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHEM-) CHEMOCENTRYX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-APP 2001; 2001W1-8812950.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse/human hybridkine mMNC/hMCP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /nofe= "Caresponds to residues 11-76 of hmpp2
(aAG78390)"
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Best Local Similarity

100.89. 100.0%;

Score 25; Fred. No.

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Length 77,

Sequence

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RESULT 15
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Best Local Similarity
Thickes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; mouse; monocyte chemotactic protein 2; hMCP2; MCP2; mCP0; mMNC; chimeric chemokine; immune response; cytostatic; antimicrobial; immunostimulant; vaccine; cancer; breast cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric chemokine mMDC/hMCP2 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG68358 standard; peptide; 77 AA
                                                                                                                                                                                                                                                         composition containing an antigen-presenting cell chemotaxin (APC-chemotaxin), where the APC-chemotaxin is a chemokine polypeptide, its variant, or a polynucleotide encoding the chemokine polypeptide or its variant. The APC-chemotaxin has cytostatic, antimicrobial and immunostimulant activities, and can be used in vaccine production. The method can be used for inducing or enhancing an immune response. The providing protection from exogenous foreign infectious pathogenic or for providing protection from exogenous foreign infectious pathogenic agents prior to expected or possible exposure, or to induviduals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric - Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carcinoma; melanoma; tumour; hybrikine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inducing an immune response to an antigen to confer non-specific protection while the body is generating the adaptive response,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schall TJ. Talbot D:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHEM-) CHEMOCENTRYX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-AFR-1000; 2000US-198839F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprises administering a composition containing an antigen-presenting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI: 2002-049246/06.
                                                                                                                                                                         displaying symptoms of exposure. The method may be used to treat cancers e.u. breast cancer. lung cancer, carcinomas, melanomas, and tumours. The present sequence represents an exemplary chinoric chemokine desimated mmMC/LMCP2. Which is given in an example from the present invention for the design of hybrikines (chimoric chemokines).
                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a method for inducing an immune response to an antigen in a subject. The method comprises administering a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5; Fig 2; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell chemotaxin
                                                                                                                                         Sequence
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26 LESYT 30
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Search completed: April 8, 20(3, 12:01:37 Job time: 45.3333 secs

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    protein search, using sw model

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     Listing first 45 summaries
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US-08-436-664-20
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US-08-7604-20
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Sequence 37, Appl
Sequence 37, Appl
Sequence 34, Appl
Sequence 32, Appl
Sequence 34, Appl
Sequence 32, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08470323A Patent No. 6031080 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20. Application US/08480449 Patent No. 5688927
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EARLIER APPLICATION NUMBER: DT
EARLIER FILING DATE: 1994-09-14
EARLIER APPLICATION NUMBER: GB 9318984.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: CHEMOTACTIC CYTOKINE FILE REFERENCE: 550-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: WILLIAMS, TIMOTHY J.
APPLICANT: JOSE, PETER J.
APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER FILING DATE: 1993-09-14 EARLIER APPLICATION NUMBER: 38 °
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER [35,68,475,313A]
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER FILING DATE: 1994-04-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: HSUAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 11
                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURPENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Godiska, Ronald APPLICANT: Gray, Patrick W. TITLE OF INVENTION: MACROPH
                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
NAME: GASS, DAVID A. REGISTRATION NUMBER: 38.153
REFERENCE, TOTACT NUMBER: 276
TELECOMMUNICATION INFORMATION:
                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 LESYT 27
                                                                                                                                                                                                                                                                        STATE: I
                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 100.0%; Score 25; DB Local Similarity 100.0%; Pred. No. 40;
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                                                                                         FILING DATE: 530
                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                             APPLICATION NUMBER: US/08/480,449
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                                                                                                                                                                                                                                                          60606-6402
                                                                                                                                                                                                                                                                                                                chicago
                                                                                                                                                                                                                                                                        Illinois
United States of America
                                                                                                                                                                                                                                                                                                                                 E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
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                                                                                                                                                                                                                                                                                                                                                                                                         MACROPHAGE DERIVED CHEMOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SE 940x5400 2
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US-08-716-188-3
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                                                                        US-08-716-188-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08715158 Patent No. 5908829
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Best Local Similarity 100
Thehes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
Query Match 100 0%, Score 25, DB Best Local Similarity 100.0%; Pred. No. 41; Matches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 76 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: KELLY,
                                                                                                                                                                                          TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: USE OF MCP-1 FOR INDUCING RIPENING OF TITLE OF INVENTION: THE CERVIX NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-105/MS-DOS
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: GR 9406463.1 FILING DATE: 31-MAR-1+94 ATTORNEY/AGENT INFORMATI-N:
                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P1/3
FILING DATE: 31-MAR-1/95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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"TTTX: 25-3856
                                                                                                                                                           SEQUENCE CHAPACTERISTICS:
LENGTH: 76 amino acids
                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION: 703-816-4(91
                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHERENT APPLICATION DATA APPLICATION NUMBER: U.
                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_fea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LESYT 5
                                                                                                                                                                                                                                                                                 NAME: SADOFF, B.J. REGISTRATION NUMBER:
                                                                                                            TOPOLOGY:
                                                                                                                       STRANDEDNESS:
                                                                                                                                             TYPE:
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100 0%; Pied. No. 41;
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 Mismatches

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                                         DB 2; Length 76;
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            0; Gaps
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1 LESYT 5

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US-08-479-603-20
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              Sequence 20. Applicat
Fatent No. 6320023
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/558
FILING DATE: 16-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: GASS, DAVID A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: F10ppy disk
COMPUTER: TRM PC compatible
OPERATING SYSTEM PC-POS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/660.542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Godiska, Kondiu
APPLICANT: Gray, Patrick W.
IITLE OF INVENTION: MACFORMAGE DEPIVED CHEMOKINE AND CHEMOKINE
TITLE OF INVENTION: ANALOGS
TITLE OF INVENTION: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: U. STREET: U. Chicago CITY: Chicago TTATE: Illinois
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/CHOCKET NUMBER 27:
TELECOMMUNICATION INFORMATION:
TELECHONE 312/474-6300
TELECHON: 312/474-0448
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PRIOR APPLICATION DATA:
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                                                                                                                                                      25 LESYT 29
                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sin
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60606-6402
                                                      Application HS/08479603
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Godiska, Ronald
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TELERAX: 25/3856
INCOMMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS
FRUITH: 76 acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100 0%: Score 25; DB Best Local Similarity 100.0%, Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         APPLICANT: Hawkins, Phillip F. APPLICANT: Bandman, Olga APPLICANT: Seilhamon
                                                                                                                                                                                                               TITLE OF INVENTION: EXPRESSED CHEMOKINES, TITLE OF INVENTION: PROUNTION AND USES NUMBER OF SEQUENCES; 12
CORRESPONDENCE ARCOND
SOFTWARE: FastSEQ Vers on 1.5 CURRENT APPLICATION DATA:
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPUTED AS A COMPUTER SYSTEM. FO CALLES AS LOS SOFTWARE PALENTIA REGIONS #1.0. Version #1.25 CURRENT APPLICATION DATA:
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TITLE OF INVENTION: MACHIPHAGE DERIVED CHEMOKINE NUMBER OF SEQUENCE: 24
CORPESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
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                               OPERATING SYSTEM:
                                                                                                                                                           STREET: 3174 Por
CITY: Palo Alto
                                                      COMPUTER:
                                                                                                                         COUNTRY:
                                                                                                                                              STATE:
                                                                                                                                                                                                ADDRESSEE:
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STRANDEDNESS: sir
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
COMPUTER: II
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STATE: Illinoi
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3174 Porter Drive
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US/08/347 492B

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Matches 5: Conserv
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FILING DATE: 25-WOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 25/203
FILING DATE: 07-SEP-1994
FILING DATE: 07-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE: Peptide
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLOVE. GI 126829
8-447-4928-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/TOCKET NIMBER. PF:0024
TELEPOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 9:
                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 05-0CT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BANDMAN, OLGA
APPLICANT: COLEMAN, ROGER
APPLICANT: STUART, SUSAN G.
TITLE CF INVENTION. NEW CHEMOKINE EXPRESSED IN EOSINOPHILS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TIBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
             SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER. USZOS/421,144A
                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Luther, Barbara REGISTRATION NUMBER: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: INCYTE PHARMACEUTICALS, INC
STREET: 3174 Forter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 LESYT 30
                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                          REGISTRATION NUMBER: 339
REFERENCE/DOCKET NUMBER.
                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY .
STRANDEDNESS:
                                                                                     TELEFAX:
                                                                                                      TELEPHONE:
                                                                                                                                                                               NAME:
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                                                                                     415-852-0195
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05-00T-1994
                                                                                                        415-855-0555
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 single
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100.0%; Fred. No. 42;
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: MOLECULE TYPE: protein US-08-421-144A-6
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                                                                                               US-Ū8-798-143-9
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Best Local Similarity 100. 6. Pred. No. 42;
Matches 5. Consorvative or Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Wilde, Craig
                              Matches
                                                              Query Match
                                                Best
                                                                                                                                                                                                                                                        TELEFAX: 415-852-0195
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APPLICANT: Hawkins, Dige
APPLICANT: Bendman, Olge
APPLICANT: Seilhamer, Jeitrey J.
APPLICANT: Seilhamer, Jeitrey J.
TITLE OF INVENTION: EXPHENSED CHEMOKINES, THEIR
TITLE OF INVENTION: PROPERTION AND USES
NUMBER OF SEQUENCES: 12
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA
                                                                                                           IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: GI 126829
                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 05-00T-1/94
ALTOKNEY/AGENT INFORMATI 9:
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                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS LENGTH: 77 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Palo Alto
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                              Local Similarity hes 5; Conserv
                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                        NAME:
                                                                                                                                                                                            STRANDEDNESS:
 1 LESYT 5
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                         10: 0%; Score 25; DB nilarity 10: 0%; Pred. No. 42; Conservativ: 0; Mismath
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26 LESYT

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APPLICANT: LEDER, PHILIP
APPLICANT: GARGIA, EDUARDO
TITLE OF INVENTION: ECTAXIN: AN FOSINOFHIL CHEMCATTRACTANT
FILE PETERNICE: 00383/025002
CURRENT APPLICATION NUMBER: (85/04/%, 887A
CURRENT EILING DATE: 1999-08-04
PRIOR FILING DATE: 1999-08-04
PRIOR FILING DATE: 1995-06-22
PRIOR FILING DATE: 1995-06-22
PRIOR FILING DATE: 1995-09-01
PRIOR FILING DATE: 1998-06-16
PRIOR FILING DATE: 1998-06-16
NUMBER OF SEC IC NOS. 27
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: ORGANISM: Homo sapions
US-09-366-997A-12
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US-04-227-357-499
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APPLICANT: Fischer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE. P.
SEQ ID NO 12
LENGIH: 77
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Best Local Similarity 100.0%;
Matches 5 Conservation 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Fischer et al. TITLE OF INVENTION: 123 Human Segreted Proteins FILE REFERENCE: PZ010Pl
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EARLIER APPLICATION NUMBER, 60/051,916 EARLIER FILING DATE: 1997-07-08 EARLIER APPLICATION NUMBER, 60/051,940 EARLIER FILING DATE: 1997-07-08 EARLIER APPLICATION NUMBER: 60/051,918 EARLIER FILING DATE: 1997-07-08
                                                                                                                                                     EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,932
EARLIER FILING DATE: 1997-07-08
                                                                                                                                                                                                                                  EARLIER FILING DATE: 1997-07-08 EARLIER APPLICATION NUMBER: 60/051,931
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EARLIER APPLICATION NUMBER: 60/052,732
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EARLIER APPLICATION NUMBER: 50/051,925
EARLIER FILING DATE: 1997-07-08
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Fred. No. 42:
0 Mismatches
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US-08-951-871-6
; Segmence 6, Application US/08451871
; Patent No. 5866398
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: ORGANISM: Homo sapiens
rg:09:227-357-488
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                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local (
                                                                                                                                       GENERAL INFORMATION:
APPLICANT: XI, SHUANG-YONG
APPLICANT: XIAO, JIAN-PING
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EARLIER FILING DATE: 1997-09-12
EAPLIER APPLICATION NUMBER: 6070
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EARLIER APPLICATION NUMBER
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EARLIER APPLICATION NUMBER 69/08-18
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EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,950
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EARLIER FILING DATE: 1997-08-18
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EARLIER FILING DATE: 1097-08-18
EARLIER FILING DATE: 1097-08-18
EARLIER APPLICATION NUMBER: 6070
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EARLIER FILING DATE: 1997-09-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ∭ ID NÓ 488
LENGTH: 255
                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
                                    CORPESPONDENCE ADDRESS:
                                                            NUMBER OF SECUENCES.
                                                                                                                                                                                                                                                                                                                              163 LESYT 167
                                                                                                                                                                                                                                                                                                                                                                                                          y Match 100 0%; Score 25; DB 4;
Loral Similarity 100 0%, Fred. No. 1.4e+02;
hes 5. Conservative 0; Mismatches 0;
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FILING DATE: 1997-68-18
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APPLICATION NUMBER 60/0
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32 Tozer Road
                   New England Biolabs, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1997 - 37 - 08
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                                                                                                METHOD FOR CLONING AND PRODUCTION THE HELL RESTRICTION ENDOUGLEASE IN E.
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; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-951-871-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-09-134-001C-4633
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                                                                                                                                                           US-09-134-001C-4633
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: LYND DOUGETE-Stamm et al
APPLICANT: LYND DOUGETE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SECUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CUBRENT APPLICATION HUMBER - US/09/134,001C
CUBRENT EILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER - US 60/064-964
PRIOR APPLICATION NUMBER - US 60/064-964
PRIOR ETLING DATE: 1997-11-08
PRIOR ETLING DATE: 1997-08-14
NUMBER OF SEO ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 463s, Application 05/091340010 patent No. 6380370
                                                                                                                                                                                                                 SEQ ID NO 4633
LENGTH: 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 5, Conserv
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                                                                                                 Best Local Similarity
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                                                                                                                                                                           ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 978-927-5054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216 LESYT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Beverly STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY .
291 LESYT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 978-927-1705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Williams, Gregory D
REGISTRATION NUMBER: 30901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER.
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                                       1 LESYT 5
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                                                                            5; Conservative
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                                                                                               100.0%; Score 25; DB 4: 100.0%; Pred. No. 3e+02;
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    Mismatches

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                                                                                Mismatches
                                                                                                                        DB 4: Length 538;
                                                                                0;
                                                                                  0;
                                                                                  Gaps
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PATENT NO. 5180808

PATENT NO. 5180808

APPLICANT: RUOSLAHTI, ERKKI I.

TITLE OF INVENTION: VERSI-AN CORE PROTEIN, NUCLEIC ACID

SEQUENCES ENCODING THE SAME, NUCLEIC ACID PROSES, ANTI-VERSICAN

ANTIBODIES, AND METHODS OF DETECTING THE SAME

NUMBER OF SEQUENCES: 4

NUMBER OF SEQUENCES: 4
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                                                                                                                                                                                                                                                    : OTHER INFORMATION: Description of Artificial Sequence: Symbolic to J. OTHER INFORMATION: Sequence: 05-09-562-737-116
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US-09-562-737-116
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                                                                                       Db
Search completed: April- 8. . . . . . . . Job time : 16.4167 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Pat
SEQ ID NO 116
LENGTH: 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 116, Application US/09562737 Patent No. 6428967
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Matches 5; Conser
                                                                                                                                                                        Matches
                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Faceptor Signaling Fathways
FILE REFERENCE: UTSW0708
CORRENT AFFLICATION NUMBER 18,79,562,737
CUPPENT FILING DATE: 2000 05-01
NUMBER OF SEQ ID NOS: 132
CORRENANCE DESCRIPTION 11
                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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                                                                                     86 MESYT 90
                                                                                                                                                                        Local Similarity 80.
Les 4; Conservative
                                                                                                                              1 LESYT 5
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80.1%;
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100 (%; Pred. No. 1.4e+03;
tive 0; Mismatches 0;
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                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                           Score 23; DB 4; Length 185; Fred. No. 3e+02;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                         April 9 2003 12:01:50; Search time 9:15:62 Searchs (without alignments) 33:347 Million coll updates/see
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Gapon 10 0 , Capext 0 5
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1: /cgn2_6/ptodata///pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata///pubpaa/US08_NEW_PUB.pep:*
3: /cgn2_6/ptodata//pubpaa/US08_NEW_PUB.pep:*
3: /cgn2_6/ptodata//pubpaa/US08_ECH6-MW_PUB.pep:*
4: /cgn2_6/ptodata//pubpaa/US07_PUB-MW_PUB.pep:*
6: /cgn2_6/ptodata//pubpaa/US07_PUB-MW_PUB.pep:*
7: /cgn2_6/ptodata//pubpaa/US08_PUB-MW_Pep:*
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11: /cgn2_6/ptodata//pubpaa/US08_PUB-MW_PEP:*
12: /cgn2_6/ptodata//pubpaa/US08_PUB-MW_PEP:*
13: /cgn2_6/ptodata//pubpaa/US08_PUB-MW_PEP:*
14: /cgn2_6/ptodata//pubpaa/US08_PUB-MW_PEP:*
15: /cgn2_6/ptodata//pubpaa/US08_PUB-MW_PEP:*
16: /cgn2_6/ptodata//pubpaa/US08_PUB-MW_PEP:*
17: /cgn2_6/ptodata//pubpaa/US08_PUB-MW_PEP:*
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19: /cgn2_6/ptodata//pubpaa/US08_PUB-MW_PEP:*
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11: /cgn2_6/ptodata//pubpaa/US08_PUB-MW_PEP:*
12: /cgn2_6/ptodata//pubpaa/US08_PUB-MW_PEP:*
13: /cgn2_6/ptodata//pubpaa/US08_PUB-MW_PEP:*
14: /cgn2_6/ptodata//pubpaa/US08_PUB-MW_PEP:*
15: /cgn2_6/ptodata//pubpaa/US08_PUB-MW_PEP:*
16: /cgn2_6/ptodata//pubpaa/US08_PUB-MW_PEP:*
17: /cgn2_6/ptodata//pubpaa/US08_PUB-MW_PEP:*
18: /cgn2_6/ptodata//pubpaa/US08_PUB-MW_PUB-MW_PEP:*
18: /cgn2_6/ptodata//pubpaa/US08_PUB-MW_PUB-MW_PUB-M
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Prel N is the burlet of results predicted by charge to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result	score	Query	Query Match Length DB	Ē.	ID	Description
1	ta i		7. 1	= 1	137-12-454-351-450C2	Sequence 4 source.
€.	<u></u>	100 0	1 44	5	08-09-195-457-6	Sequence E. Appli
ىيا	t) N	100.0	, <del>1</del>	ů.	US-09-792-793A-21	Sequence 11, Appl
4	ŁJ Л		77	ю	*HS - 68 - 42 7 - 434 - 17	Sequence 17, App.
5	t) (n	1000	11	4	98-10 057 275-10	Sequence 10, Appl
a)	F) P,		1	29	05-54-844-744A-24	Wind and the Section
-1	t3 (n	100.0	1	ټ	US-09-920-137A-10	Cequetice 10, Appl
œ	25	100.0	77	10	118-04-844-745A 24	Cognorno 24. April
۰	25	100 5	109	٤	US-10-033-067-1	Sequence 1, Appli
16	1.1	*		4.1	日の・100・7×1×3×3×3×3×3×5	STREET, TOWNS AND
11	1.5 1.0	1? 			08 - 09 - 733 - 675 - 601	Sequence 201, App
12	r)	1000	# · ·	÷	HS 5 1 875 113A 184	Serguence 184, App
13	25	100.0	255	œ	US-09-983-802-488	Sequence 488, App
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E OT	25	100.0	467	۲	US-10-160-501-14	Sequence 14 April
16	<b>₽</b> 5	100	÷	÷	TENDER TO COLOR	Security of Alexander
1.3	25	10000	4 # 9	10	US-09-925-400-1170	Sequence 1170, Ap
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14	N)	ું દુર	000	Ç	US-09-808-216-4	Sequence 4, Appli

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US-10-176-758-600	US-10-174-590-500	US-09-997-653-225		US-09-989-724-225	US - 09 - 993 - 687 225	US-09-991-181-225	US-09-990-436 225	US-09-989-730-225	1.8 .03 .33 . 444 .22 E	46-09-984-725-225	US-09-989-293A-225	98-29-992 598-225	40 - 45 - 507 - 708	US-10-108-605-147	US-10-150-648H-30	19-04-854-751-45840	US-10-150-648B-33	S.1138.158.19	US-09-864-761-45367	US-09-862-179A-19	US-09-945-166A-6	US-10-161-499-2	01 743-706-60-50	115-04-815-242-10668	RAE - 1842 - [118 - 1843
Sequence 500, App	•	Sequence 225, App							`	Serpiones 225. App	Sequence 225. App.		Sequence 708, App	Sequence 147, App	Sequence 30, Appl	sequençe 45840, A	Sequence 43, Appl	Sequence 19 Appl	Sequence 45367, A	Serpance 19. Appl	seguence 2, Appli	Sequence 2, Appli	Sequence 30, Appl	Sequence 10668, A	sequence 398, App

## ALIGNMENTS

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MEY DSEFT

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; Sequence 6, Application US/09195457
; Patent No. US20020081623A1
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                                                                                             RESULT 3
US-09-792-793A-21
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
OTHER INFORMATION: EST_HUMAN HIT: AA357020.1, EVALUE 1.00e-07
1-09-864-761-46020
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 46020
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                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 6
LENGTH: 74
                                   GENERAL INFORMATION:
                                                     Sequence 21, Application US/09792793A Patent No. US20020168370Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: WILLIAMS, TIMOTHY J. APPLICANT: JOSE, PETER J. APPLICANT: GRIFFITHS-JOHNSON, D. APPLICANT: HSUAN, JOHN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER US 09/774.203 PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608.408
PRIOR FILING DATE: 2000-06-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/214,687
                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: POT/SE44/02000
PRIOR PILING DATE: 1994-09-14
PRIOR APPLICATION NUMBER: GB 9318984.3
PRIOR FILING DATE: 1993-09-14
PRIOR APPLICATION NUMBER: GB 94086902.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/195/457
CURPENT FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 08/470,323
PRIOR FILING DATE: 1995-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: FILE REFERENCE: 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens FEATURE:
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APPLICANT: Coggins, Philip
                  APPLICANT: McDonald, John R.
                                                                                                                                                                                                                                                                                                                                                           ORGANISM: human
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Local Similarity 100.0%;
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                                                                                                                                                                                                              1 LESYT 5
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Pred. No. 37;
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US-08-927-939-17
; Sequence 17, Application US, 6927939
; Patent No. US20010006640A1
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US-08-927-939-17
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US-10-057-275-10
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LENGTH: 77
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                                                                                                                                                                                                                                                                               Sequence 10, Application US/10057275 Patent No. US20020155645A1 GENERAL INFORMATION:
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Matches 5, Conserv
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CURKENT AFPLICATION HUMBER: 18/08/927.939
CURRENT FILING DATE: 1997.0-11
NUMBER OF SEQ ID NOS: 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Grainger, David | APPLICANT: Tatalick, Lauen M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE, fastSEQ for Wind-we Version 3.0
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nes 5; Conserv
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               ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                         TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCKEAS
                                                                                                                                                                                                                                                                   APPLICANT: Coleman, Roger
                                                                                                                             ADDRESSEE: Incyt- Pharmaceuticals, Inc
STREET: 3174 Poiter Drive
COMPUTER: IBM Compatible
                                                                       COUNTRY: U.S.
                                                                                           STATE: CA
                                                                                                           CITY: Palo Alte
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100 %, Fred. No. 39:
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RESULT 7
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: ORGANISM: Homo sapiens
US-09-834-794A-24
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: Sequence 24, Application บระกษัท34794A
: Publication No. บระกบัวกับสะสารสา
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                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/071,899
PRIOR FILING DATE: 1998-01-20
PRIOR APPLICATION NUMBER: 60/092,155
PRIOR FILING DATE: 1998-07-09
                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/146,580 PRIOR FILING DATE: 1998-09-03
                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/04/H44, 794A CURRENT FILING DATE: 2001-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Detection and Treatment of Breast Cancer FILE REPERENCE: 3380/11127 \cdot 084
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                                                                                                         y Match
Local Similarity 100.0%; Pred. No. 39;
hes 5; Conservative 0; Mismatches
                                               26 LESYT 3
                                                                                   1 LESYT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: LULber, Barbara J.
REGISTRATION NUMBER: 33,954
PFREPENCE/POCKET NUMBER: FF-5027 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/057,275
FILING DATE: 25-Jan-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 77 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Jana, Frustaci
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CLONE: MCP-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-852-0195
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Pred, No. 39;
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ITILE OF INVARION: INTERCTION and Treatment of Hieast Cancer
FILE REFERENCE: 3380/11127-U: (17.834,795A)
CUPPENT APPLICATION NUMBER: (17.73,834,795A)
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: (19.146,580)
PRIOR FILING DATE: 1998-09-00
PRIOR APPLICATION NUMBER: (19.771,899)
PRIOR APPLICATION NUMBER: (19.771,899)
PRIOR FILING DATE: 1998-01-20
SOFTWARE: Patentin version 3.1
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APPLICANT: Lyn, Dysten
APPLICANT: Jana, Frustaci
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: Publication No. US200300497/5A1
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MOLECULE TYPE: pe
IMMEDIATE SOURCE:
LIBRARY: GenBar
CLONE: MCP-2
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TELEPHONE: 415-855-055
TELEPAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 10-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA APPLICATION NUMBER: US
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APPLICANT: Bandman, Olga
APPLICANT: Wilde, Craig 1.
TITLE OF INVESTIGAL PROPERTY OF THE PROPERTY OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 LESYT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%:
Local Similarity 100.0%:
es 5; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 77 amino acids
TYPE: amino acid
STRANDEDNESS: single
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SOFTWARE: FastSEQ Version 1.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
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CITY: Palo Alto
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ZIP: 94304
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STREET: 3174 Porter Drive
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Pred. No.
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; ORGANISM: Homo sapiens
US-09-834-795A-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEATURE:
NAME/KEY misc_feature
OTHER INFORMATION: Incyte 15 No. 0520020164704A1 965517CD1
US-10-033-067-1
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Patent No. US20020164704Al
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APPLICANT: Coleman, Roger
APPLICANT: Hillman, Jenii
APPLICANT: AU-Young, Jani
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APPLICANT: AU YOUNG, Janie

ITITLE OF INVENTION: MOVEL HUMAN MONOCYTE CHEMCTACTIC PROPROTEIN

FILE REFERENCE: PF-0069-1 CON

FILE REPERENCE: PF-0069-1 CON

CURRENT APPLICATION NUMBER: US/10/033.067

CURRENT FILING DATE: 2001-10-26

PRIOR APPLICATION NUMBER: 08/583.655

PRIOR APPLICATION NUMBER: 08/583.655

PRIOR APPLICATION NUMBER: 08/583.655

PRIOR FILING DATE: 1996-07-15

NUMBER OF SEQ ID NOS: 7

NUMBER OF SEQ ID NOS: 7

NUMBER OF FERL Frogram

SOFTWARE: PERL Frogram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-754-858-875
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LENGTH: 109
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Best Local S
                                                                                                                                                                                                                                                                  PAPELICANT: Rosen et al.
APPLICANT: Rosen et al.
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
TITLE PEFFRENCE: PIT32
FILE PEFFRENCE: PIT32
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
CURRENT FILING DATE: 2001-01-17
OFFICE APPLICATION data removed - refer to PALM or file wrapper
Prior application data removed - refer to PALM or file wrapper
PRIOR APPLICATION NOS: 1510
NUMBER OF SEQ ID NOS: 1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 875, Application US/09764868 patent No. US20020168711A1
                                                                                                                                                                                                 SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 875
LENGTH: 151
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ORGANISM: Homo sapiens
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                           LOCATION: (117)
LOCATION: (117)
LOCATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (127)
LOCATION: (127)
                                                                                                                  NAME/KEY: SITE
                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 LESYT 62
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100.0%: Pred. No. 55:
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US-09-764-868-875

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US-09-791-279-201
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AFFLICANT: Lind Peter
TITLE OF INVENTION: No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Vogeli, Gabrie APPLICANT: Wood, Linda S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000 PRIOR APPLICATION NUMBER: FRICE FILING DATE: 2000
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                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE.
                                                                                                                                                                                                          sequence 184, Application US/09895913A Patent No. US20020160456A1
                                                                                  APPLICANT: Kleanthous, Harold AppLICANT: Al-Garawi, Amel AppLICANT: Miller, Charles
                            Applicant: Tomb, Jean Franco Applicant: Comen, Raymond \rho.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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TITLE OF INVENTION: Identification of Polynucleotides
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                                                                                                                                                                                                                                                                                                                                                                                                    155 LESYT 159
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                                                               Miller, Charles
Tomb, Jean Francois
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GENERAL INFORMATION:
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COURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,357
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/13684
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OPDANISM: Helicobacter pylori
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APPLICAMN: OZAKI, AKIO
TITLE OF INVENTION: NOVEL PHANDCLEOTIDES
FILLS PREPERNE: 249-125
CTEPENT AFFECTATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 99/377484
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SOFTWARE: PATENTIA VET. 3.0
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US-09-738-626-6675
Sequence 0075, Application Hs/
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APPLICANT: NAKAGAWA
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YOKOI, MARUHIKO
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. ORGANISM: Corynebacterium glutamicum 08\text{-}09\text{-}738\text{-}626\text{-}6675
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PRIOR APPLICATION NUMBER: US 09/838,573

PRIOR APPLICATION NUMBER: US 60/197,747

PRIOR APPLICATION NUMBER: US 60/197,747

PRIOR APPLICATION NUMBER: US 60/197,747

PRIOR PRIOR FILING DATE: 2000-05-18

PRIOR PRILING DATE: 2000-05-26

PRIOR PRILING DATE: 2000-05-26

PRIOR PRILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 60/207,640

PRIOR APPLICATION NUMBER: US 60/207,640

PRIOR APPLICATION NUMBER: US 60/207,640

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 60/207,961

PRIOR APPLICATION NUMBER: US 60/205,961

PRIOR APPLICATION NUMBER: US 60/205,961

PRIOR APPLICATION NUMBER: US 60/207,506

PRIOR PRIOR PILING DATE: 2001-05-29

PRIOR APPLICATION NUMBER: US 60/207,506

PRIOR FILING DATE: 2001-05-26

PRIOR FILING DATE: 2001-05-26

PRIOR PRIOR PRIOR DATE: 2001-05-26
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LENGTH: 332
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Best Local Similarity
Matches 5: Conserv
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                                                                                                                                                                                                                                PRIOR FILING UALE: 2001-05-17
PRIOR APPLICATION NUMBER: US 09/870,110
PRIOR APPLICATION NUMBER: US 60/207,650
PRIOR APPLICATION NUMBER: US 60/207,650
PRIOR APPLICATION NUMBER: US 09/907,509
PRIOR FILING DATE: 2001-07-16
PRIOR FILING DATE: 2001-07-14
PRIOR FILING DATE: 2001-07-14
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,425
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/218,581
PRIOR APPLICATION NUMBER: US 60/318,581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Meyers, Rachel E.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: NOVEL HUMAN 39228, 21956, 25856, 22144, 8701,
TITLE OF INVENTION: NOVEL HUMAN 39228, 21956, 25856, 22144, 8701,
TITLE OF INVENTION: MOLECULES AND USES THEREFOR
FILE REFERENCE: MNI-250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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CURRENT FILING DATE: 2002-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR ETILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,449
PHIOR ETLING DATE: 2000-05-19
                                                                                                SEQ ID NO 14
                                                                                                                                                         PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 LESYT 238
                                                                                                                         SOFTWARE: FastSEQ Version 4.0
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ORGANISM: Homo sapiens
                                                                LENGTH:
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US-10-160-501-14

Query Match
Best Local Similarity 100.0% Score 25; DR 9; Length 467;
Best Local Similarity 100.0% Pred. No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps
Matches 6; Mismatches 0; Indels 0; Gaps
Mismatches 0;
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           duence.
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           Pred. No. is the number of results predicted by chance to have a score areater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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           oldsymbol{\alpha}
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Query
Match Length DB
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         Genfore version 5 1 4_p5_4578 Copyright (e) 1993 - 2003 Compugen Ltd.
      US-09-134-001C-3833
US-09-134-001C-3033
US-08-855-6241-15
US-08-855-6241-15
US-08-855-6241-15
US-08-955-263-16
US-08-955-263-16
US-08-955-264-117
US-08-955-284-117
US-08-856-8241-19
US-08-955-950-12
US-09-695-950-12
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Sequence 9, Appli
Sequence 15, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 18, Appli
Sequence 19, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 2, Appli
Sequence 2, Appli
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Sequence 3, Appli
Sequence 3, Appli
Sequence 12, Appli
Sequence 13, Appli
Sequence 14, Appli
Sequence 15, Appli
Sequence 16, Appli
Sequence 17, Appli
Sequence 18, Appli
Sequence 19, Appli
Sequence 19, Appli
Sequence 19, Appli
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Sequence 3015, Ap
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RESULT 2 US-99-144-001C-3015  Sequence 3015, Application US/09144001: Patent No. 6380370  GENERAL INFORMATION: APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC AND AND ACID SEQUENCES ELIAITM, TO STAFBYLDECC TITLE OF INVENTION: EPIDERMIDIS FOR TAIMSSTICS AND THEPAPEUTICS  PILE REPERENCE: GTC-007 COPPENT AFFILIATION NUMBER: US 50,053,7134 vol? CORRENT FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-08-14 PRIOR FILING DATE: 1997-08-14 PRIOR FILING DATE: 1997-08-14 PRIOR FILING DATE: 1997-08-14 SEC ID NO 3015 LENGTH: 703 TYPE: PRI	Ouery Match 88.9%; Score Q; DB 4; Length 204; Best Local Similarity 71.4%; Pred. No. 12; Matches 5; Conservative 2; Mismitches 0; Indels 0) Gaps 0; Oy 1 IKEYFTS 7 :	RESULT 1  US-09-134-001C-3833  Sequence 3833, Application US/09134001*  Patent NO. 6380370  GENERAL INFORMATION: AFFLICART, Lynn Doucette-Stamm et al AFFLICART, Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACTD AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: NUCLEIC ACTD AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: PRINFFWAILS FOR TAKEN STITES AND THEPAPPUTICS  FIRE PEPEPAMOE: GIC-002  FIRE PEPEPAMOE: GIC-002  CURPENT ELLING LATER 1998-08-13  FRICE ALFELICATION NUMBER: US 60/055.7**  PRIOR APPLICATION NUMBER:	ALIGNMENTS	28 27 75.0 62 4 US-09 144 474 486 Sequence 14. Appl 30 27 75.0 66 1 US-08-482-111-14 Sequence 14. Appl 30 27 75.0 66 1 US-08-482-111-14 Sequence 14. Appl 31-2 75.0 68 2 US-08-944-193-2 Sequence 2. Appl 18-32 27 75.0 68 2 US-08-944-187-17 Sequence 17. Appl 18-2 75.0 68 2 US-08-944-187-17 Sequence 17. Appl 18-2 75.0 68 2 US-08-944-183-1 Sequence 17. Appl 18-2 75.0 68 3 US-08-44-183-1 Sequence 17. Appl 18-2 75.0 68 3 US-08-44-183-1 Sequence 17. Appl 18-2 75.0 68 4 US-08-84-183-1 Sequence 17. Appl 18-2 75.0 68 4 US-08-84-183-1 Sequence 17. Appl 18-2 75.0 68 4 US-08-84-183-1 Sequence 17. Appl 18-2 75.0 69 4 US-08-84-183-1 Sequence 18. Appl 18-2 75.0 69 4 US-08-84-183-1 Sequence 18. Appl 18-2 75.0 69 4 US-08-84-182-2 Sequence 18. Appl 18-2 75.0 A
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ORGANISM: Staphylococcus epidermidis 09-134-001C-3015
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08-856-841-9
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                                                                                                                                                                                                                                                                                                         TELEX: NONE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 27,224
REFPENCE, TOYCKET NUMBER: LFF-N222-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA: APPLICATION NUMBER 08/08/856,841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MANERED MÓ12
TITLE OF INVENTION: OR POLYPEPTIDES PROM THE PARVOVIRUS R19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                      FRAGMENT TYPE: INTERNAL ORIGINAL SOURCE: SERUM FROM PATIENT WITH ACUTE IMMEDIATE SOURCE: GENETICALLY ENGINEERED PEPTIDE
                                                                                                                                                                         DESCRIPTION: PEPTIDE HYPOTHETICAL: N/A
                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: DESUGSEA FILING DATE: 8-FEBRUARY-1990 AITORNEY/AGENT INFORMATION: NAME: ROBINSON, WILLIAM R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/01
FILING DATE: 16-MARCH-1994
APPLICATION NUMBER: US 07/01
FILING DATE: 4-AUGUST-1992
APPLICATION NUMBER: PCT/0F40
FILING DATE: 8-FEBRUARY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                      FEATURE
                                                                                     POSITION IN GENOME: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 KDYFTS 200
                                                                                                                                                              ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: AT&T - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                     TYPE:
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                                                     NAME/KEY
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IDENTIFICATION METHOD:
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                                                                                                                                                              N/A
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                                                                                                                                                                                                                                    LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: PCT/1)F41/00106
8-FEBRUARY-1991
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UMBER: US 07/917.096
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83.3%;
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                 amino acid analysis and
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Pred. No. 2.1e+02;
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                                                                                                                                                                                                                      Sequence 3, Application US/08811583
Patent No. 6218142
GENERAL INFORMATION:
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AUTHORS: COSSART, Y.E
AUTHORS: FIELD, A.M.
AUTHOPS: CANT, B.
                                                                      APPLICANT: Wassenegger, Michael
APPLICANT: Riedel, Léonhard
APPLICANT: Schiebel, Winfried
APPLICANT: Schiebel, Winfried
APPLICANT: Sanger, Heinz
TITLE OF INVENTION: NUCLEIC ACID M. 157 HLES ENCODING
TITLE OF INVENTION: POLYPEPTIDES HAVING THE ENZYMATIC ACTIVITY OF AN
TITLE OF INVENTION: RNA-DIRECTED RNA FOLYMERASE (RdRP)
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUBLICATION INFORMATION:
AUTHORS: MANIATIS, T.
AUTHORS: FRITSCH, E.F.
AUTHORS: SAMBROOK, J.
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RELEVANT RESIDUES IN SEQ ID NO:
PUBLICATION INFORMATION:
                COPPRESSIONNENCY ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americus
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RELEVANT RESIDUES IN SEQ ID NO:
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AUTHORS: WIDDOWS, D.
TITLE: PARYOVIPUS-LIKE PARTICLES IN HUMAN SERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
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AUTHORS: TOHNSON, K.S.
TITLE: SINGLE STEEP PURIFICATION OF FOLYPEPTIDES
TITLE: EXPRESSED IN ESCHERICHIA CHAI AS FUSIONS WITH
TITLE: GLITATHIONE S. TPANSFERASE
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1975
New York
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MOLECULAR CLONING
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STATE: New York COUNTRY: USA

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rs-08-856-841-15
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APPLICANT: ERWIN SOUTSCHEK
APPLICANT: MANFRED MOTZ
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SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSJEM: PC-DUS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,7
REFERENCE/DOCKET NUMBER:
                                                                                                                              CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER - US/04/Z
FILING DATE: 16-MARCH-1994
                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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MEDIUM TYPE: 3.5" FL
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ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PEPTIDES R19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 VEEYFTN 150
            APPLICATION NUMBER: PTY/CE91/99/
FILING DATE: 8-FEBRUARY-1991
APPLICATION NUMBER: DE40038262
FILING DATE: 8-FEBRUARY-1990
                                                                                         APPLICATION NUMBER: FILING DATE: 4-AUGU
                                                                                                                                                                                                                                                                                                                                                                                                        CITY: NEW YORK
STATE: NY
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                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: MS-DUS Version 6.2
                                                                                                                                                                                                                                                                                                               COMPUTER:
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TOPOLOGY: 11
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ATET - IBM COMPATIBLE
CYSTEM AS-DES VOCASION
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4-AUGUST-1992
UMBER: FTT/CE91/90108
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; PUBLICATION DATE: RELEVANT RESIDUES IN SEQ ID NO: US-08-856-841-15
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HYPOTHETICAL: NA
ANTI-SENSE: N/A
TYPE: INTERNAL
                                                                                                                                                                                                                                                FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 1".
PUBLICATION INFORMATION:
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PUBLICATION INFORMATION:
AUTHORS: COSSART, Y.E.
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REGISTRATION NUMBER: 27,224
KEEPERENCE/JOCKET NUMBER: LKR-9222-A
TELECOMMUNICATION INFORMATION:
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                                                                                                                 VOLUME:
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VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS:
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                                                                                                                                                              AUTHORS: SMITH, D.B.
AUTHORS: JUHNSON, POLYPEPTIDES
TITLE: SINGLE STEP PURIFICATION OF POLYPEPTIDES
TITLE: EXPRESSED IN ESCHERICHIA COLI AS FUSIONS WITH
TITLE: GLUTATHIONE S. TRANSFERASE
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RELEVANT RESIDUES IN SEQ ID NO: 15:
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LOCATION: N/A
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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DATE: 1975
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JOURNAL: COLD SPRING HARBOR, NY
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                                                                                                                                                  TOURNAL .
                                                                                                                                                                                                                                                                                                                                                                  ISSUE:
                                                                                   1988
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WIDDOWS, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                     SAMBROOK
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(212) 557-5635
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Sequence 12, Application US/08856841 Patent No. 6274307
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Best Local Similarity 66.7%;
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MEDIUM TYPE: 3.5" FUPPY DISC
COMPUTER: AIST - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
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APPLICANT: MANFRED MOTZ
TITLE OF INVENTION: INMUNOLOGICALLY ACTIVE PEPTIDES
TITLE OF INVENTION: OP POLYPEPTIDES FROM THE PAPVOVIRUS B19
                                                                                                                                    PRAGMENT TYPE: INTERNAL OPRIGINAL SOUPCE SERUM FROM PATIFNT WITH ACHTE ORIGINAL SOURCE: INFECTION (ERYTHEMA INFECTIOSUM) IMMEDIATE SOURCE: GENETICALLY ENGINEERED PEPTIDE POSITION IN GENOME: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: DE40038262
FILING DATE: 8-FEBROARY-1990
ATTORNEY_AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGERENCY.CYCKET NUMBER: 27.224
REGERENCY.CYCKET NUMBER: LKF-5222-A
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER US/08/214,658

EILING DATE: 16-MARCH 1994

APPLICATION NUMBER: US 07/917,096

FILING DATE: 4-AUGUST-1992

APPLICATION UMBER: PEDBRUARY-1991

FILING DATE: 8-FEBRUARY-1991
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DESCRIPTION: PEPILOE
OTHER INFORMATION: PUBLICATION INFORMATION:
                                                                                                                         FEATURE:
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                                    NAME/KEY: N/A
LOCATION: N/A
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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(212) 557-5635
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                                        mass spectrometry
                                                           amino acid analysis and
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Pred. No. 1e+02;
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APPLICANT: Furuichi, Yasuhiro
APPLICANT: Hoshino, Tatsuo
APPLICANT: Kimura, Hitoshi
APPLICANT: Kimura, Hitoshi
APPLICANT: Kigası, Tatsuya
APPLICANT: Nagahashi, Yoshie
TITLE DE INVENTION: BIOTIN BIOSYNTHETI: GENES
FILE REFERENCE: Biotin Genes
CURRENT APPLICATION NUMBER: US/08/935,243A
CURRENT FILING DATE: 1997-09-22
FARIJER APPLICATION NUMBER: EP 96115543.5
EARLIER FILING DATE: 1996-09-27
NUMBER OF SEQ ID NOS. 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                      US-08-935-263-16
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                                                                                                                                                                                                                                                                  Sequence 16, Application US/08935263A Patent No. 6117669
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PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 12:
PUBLICATION INFORMATION:
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hus 4. Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAGES: 51
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PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS: SMITH, D.B.
AUTHORS: JOHNSON, K.S.
TITLE: SINGLE STEP PURIFICATION OF FOLLYPEPTIDES
TITLE: ENTRESSED IN ESCHEPTOHIA OF TAX POSIONS WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISSUE:
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1975
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MOLECULAR CLONING
A. COLD SPRING HARBOR, NY
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Pred. M. 1.1e+02:
2. Misrithhas (
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Query Match
Best Local Similarity
Thehes 4: Conserva
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JS-09-594-185-16
Sequence 16, Application US/04544185
Patent No. 636388
GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Kurthia sp.
IS-09-594-185-16
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                                                                                                                                                                                                                                                                                                                                                                                            sequence 18 Application US/08605284B Patent No. 6060271
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Best Local Similarity 57 1%; Prod. No. 1
Matches 4; Conservative 3; Mismatch
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APPLICANT: Hoshino, Tatsuo
APPLICANT: Kimura, Hitoshi
APPLICANT: Kiyasu, Tatsuya
APPLICANT: Nagahashi, Yoshie
TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
FILE REFERENCE: Biotin Genes
                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 08/935,263
PRIOR FILING DATE: 1997-09-22
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PRIOR FILING DATE: 1996-09-27
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            MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                           APPLICANT: WALEWSKI, JOSE (
APPLICANT: RECIO-PINTO, ESPERANZA
TITLE OF INVENTION: VOLTAGE SATED SOLIUM CHANNELS FROM
TITLE OF INVENTION: HUMAN PERIPHERAL NERVE
NUMBER OF SEQUENCES: 23
                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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  AFFLICATION NUMBER:
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                                                                                                                                                                             NEW YORK
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US/08/605.284B
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; Sequence 17, Application 05/08856841
; Patent No. 6274307
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Best Local Similarity (1.4
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                              INFORMATION FOR SEQ ID NO: 17:
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                                                                                          PERINTRATION NUMBER: 27,224
PEFFRENCE/OOCKET NUMBER: LKP-927/A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 387
                                                                                                                                                                    FILING DATE: 8-FEBRUARY-ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA: APPLICATION NUMBER: "E FILING DATE:
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MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: AT&T - IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
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MOLECULE TYPE: protein
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NAME: BRAMAN, SUSAN J.
                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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TELEPHONE: 716-263-1636
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                                                                 TELEPHONE:
                                                                                                                                                                                  APPLICATION NUMBER: DE400382
FILING DATE: 8-FEBRUARY-1990
                                                                                                                                                                                                                                       FILING DATE: 4-AUG
AFFLICATION NUMBER.
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TYPE: amino acid
STRANDEDNESS: not releva
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CLASSIFICATION:
                                                                                                                                   NAME: ROBINSON, WILLIAM R. PEGISTPATION NUMBER: 27,22
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                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: MS-DOS Version 5.2
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                                                               : (212) 697-3355
(212) 557-5635
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JMBER: US 07/
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71.4%;
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Pred. No. 1.4e+C2;
1: Mismatches 1: Indels
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Matches
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-08-856-841-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 17:
PUBLICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUBLICATION INFORMATION: AUTHORS: COSSART, Y.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: N/A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POSITION IN GENOME.
                                                                                                                                                                                                                                                               AUTHORS: SMITH, D.B.
AUTHORS: JOHNSON, K.S.
TITLE: SINGLE STEP PURIL
TITLE: EXPRESSED IN ESCI-
TITLE: GLUTAHHIONE S. TI
JOURNAL: GENE
201 VKDYFT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS: SAMBROOK, J.
TITLE: MOLECULAR CLONING
JOURNAL: COLD SPRING HARBOR, NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS: MANIATIS, T. AUTHORS: FRITSCH, E.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DATE: 1975
DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION
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DOCUMENT NUMBER:
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                                                                           Local Similarity
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DOCUMENT NUMBER:
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S: WIDDOWS, D.
PARVOVIRUS-LIKE PARTICLES IN HUMAN SERA
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                                                               Mismatches
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US-08-856-841-19
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                                                                                                                                                                                                                                                                                                          HYPOTHELLOW N/A
ANTI SENSE: N/A
ANTI SENSE: INTERNAL
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: SERUM FROM PATIENT WITH ACUTE
ORIGINAL SOURCE: INFECTION (ERYTHEMA INFECTIOSUM)
ORIGINAL SOURCE: GENETICALLY ENGINEERED PEPTIDE
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ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
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REFERENCE/DOCKET NUMBER: LKI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3855
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ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER US/08/
FILING DATE: 16-MARCH-1994
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DESCRIPTION: PEPTIDE
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                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY:
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                                                                                                                                                                                   PUBLICATION INFORMATION:
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COMPUTER: AT&T - LBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
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FILING DATE: 4-AUGUST-1992
APPLICATION NUMBER: PCT/DE91
FILING DATE: 8-FEBRUARY-1991
APPLICATION NUMBER: DE400382
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STATE: NY
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                                                                 AUTHORS: CANT, B.
AUTHORS: WIDDOMS, D.
AUTHORS: FARMOVLINUS-LIKE PARTICLES (N HUMAN SERA
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                                                                                                                                              FIELD, A.M.
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MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: ATST - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
              FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: SERUM FROM PATIENT WITH ACUTE
OPIGINAL SOURCE: INFECTION (EPYTHEMA INFECTIOSUM)
IMMEDIATE SOURCE: GENETICALLY ENGINEERED PEPTIDE
POSITION IN GENOME: N/A
                                                                                              MOLECULE TYPE:
DESCRIPTION: PEPTIDE
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                FILING DATE: 8-FEBRUARY-1990
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTPATION NUMBER: 27 224
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TITLE OF INVENTION: OF POLYPEPTIDES FROM THE PAPADATIONS BIG
NUMBER OF SEQUENCES: 28
FEATURE:
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FILING DATE: 8-FEBRUARY
APPLICATION
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APPLICATION NUMBER
FILING DATE: 4-AUG
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STATE: NY
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STREET: 99 FARK AVENUE
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UMBER: US 07/8
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66.7%;
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Pred. No. 2.3e+02;
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// Sequence 18, Application US/08856841
// Patent No. 6274307
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                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: ERWIN SOUTS.......
APPLICANT: MANFRED MOTZ
TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PEFTIDES
TITLE OF INVENTION: OF POLYPEPTIDES FROM THE PARVIAVIRUS BIV
NUMBER OF SEQUENCES: 28
COFRESPONDENCE APPRESS:
APPRESSEE: BROOKS HAIDT HAFFNER & SELAHUNIY
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AUTHORS: MANIATIS, T.
AUTHORS: FRITSCH, E.F.
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VOLUME:
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RELEVANT RESIDUES IN SEQ ID NO: 14:
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AUTHORS: WILDOWS, D.
TITLE: FARVOVIRUS-LIKE FARTICLES IN HUMAN SERA
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AUTHORS: JOHNSON, K.S.
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1975
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MOLECULAR CLONING
L: COLD SPRING HARBOR, NY
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66.7%;
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Pred: N. 2.4e+02:
2: Mismatches
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Matches
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SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: 3.5" FLOPRY DISC
COMPUTER: AT&T - IBM COMPATIBLE
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PPIOP APPLICATION DATA:
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DESCRIPTION: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 8-FEBRUARY-1990
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE: INTERNAL ORIGINAL SOUPCE: SEPUM FROM PATIENT WITH ACUTE ORIGINAL SOUPCE: INTERTION (ERYTHEMA INFECTIOSIN) IMMEDIATE SOURCE: GENETICALLY ENGINEERED PEPTIDE
                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: COSSART, Y.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POSITION IN GENOME:
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TELEFAX: (212) 557-5635
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
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STATE: NY
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AUTHORS: CANT, B.
AUTHORS: WIDDOWS D
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                                              y Match 77.8%;
Local Similarity 66.7%;
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PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 18:
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VOLUME: I
                                                                                                                                                                      DOCUMENT NUMBER:
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                                  Mismatches
                                                Score 28; DB 4;
Pred. No. 2.4e+02;
                                                                  DB 4; Length 501;
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: TYPE: PRT
; ORGANISM: Citrus navelina var. class
US-09-413-452-2
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; Patent No. 6268195
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                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2
LENGTH: 584
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APPLICANT: Thorsoe, H.
APPLICANT: Thorsoe, H.
APPLICANT: Kreiberg, J.
APPLICANT: Suchholt, H.
TITLE OF INVENTION: PROCESS FOR STABILLZING PROTEINS IN AN TITLE OF INVENTION: ACIDIC ENVIRONMENT WITH A HIGH-ESTER PECTIN FILE PERFERCE: DYONI4 OULAPC CUPRENT APPLICATION NUMBER: 08/983364
EARLIER APPLICATION NUMBER: 08/983364
EARLIER APPLICATION NUMBER: 08/983364
EARLIER APPLICATION NUMBER: 08/983364
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EARLIER FILING DATE: 1996-07-12
NUMBER OF SEQ ID NOS: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Christensen, T.
APPLICANT: Thorsoe, H.
APPLICANT: Kreiberg, J.
APPLICANT: Buchholt, H.
TITLE OF INVENTION: PROFESS FOR STABLIZING PROTEINS IN AN
TITLE OF INVENTION: ACIDIC ENVIRONMEN: WITH A HIGH-ESTER FECTIN
FILE REFERENCE: DYOULA OGLAPC
FILE REFERENCE: DYOULA OGLAPC
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 56
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EARLIER APPLICATION NUMBER
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MEDLINE-93300846; PubMed-8314802;

Shinomura T., Nishida Y., Ito K., Kimata K.;

"CDNA cloning of PG-M. a large chondroitin sulfate proteoglycan expressed during chondroyenesis in chick limb buds. Alternative spliced multiforms of PG-M and their relationships to versican.";

J. Biol. Chem. 268:14461-14469(1993).

-i- FUNCTION: May play a role in intercellular matrix. May take part connecting cells with the extracellular matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institute. There are no restrictions on it modified and this statement is not removed. Usage by and for commencial entities requires a license agreement (See http://www.ish.sit.ch.andron.com.send an email to license@isb.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY. CONTAINS 1 IMMUNGGLOBULIN-LIKE V-TYFE DOMAIN-!- SIMILARITY: CONTAINS 2 LINK DOMAINS.
-!- SIMILARITY: CONTAINS 2 ESF-LIKE LOWAINS.
-!- SIMILARITY: CONTAINS 1 C-TYFE LECTIN FAMILY COMAIN.
-!- SIMILARITY: CONTAINS 1 SUSHI (SOP) DOMAIN.
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Eukaryota; Metazoa; Chordata; Craniata, Vertebrata, Euteleostomi,
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9031;
                     ProDum: PD000918; L1
SMART: SM00032; CCP;
                                                            pfam; pF00059; lectin_c; l
pfam; pF00084; sushi; l.
pfam; pF00193; xlink; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                            InterPro: IPR000561;
InterPro: IPR000742;
                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Secreted; extracellular matrix. ALTERNATIVE PROPURTS: At least 2 isofoles; V0 (shown hore) and V1; are produced by alternative splicing.
TISSUE SPECIFICITY: Prechandrogenic condensation area of developing limb buds.
DEVELOPMENTAL STAGE: Disappears after the cartilage development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (By similarity)
SIMILARITY, CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the regulation of cell motility, growth and differentiation. Binds hyaluronic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                           P0074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X60226; CAA42787.1;
SM00034; CLECT;
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                                                                                                                                                                                                                                                                                                                                                                                                                             LEUM.
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                     CP: 1.
                                                                                                                                                                                                                                  . ig_MHC.
. Lectin_C.
                                                                                                                                                                                                                                                                                                                    EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                         Asx_hydroxyl.
EGF-like.
                                                                                                                                                                                             Sushi_SCK_CCF.
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8

1355 KEYFTS 1360

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0
                  Matches
                         Query Match
Best Local :
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PROSITE: PS00022: EGF_L: 2.
PROSITE: PS01187: EGF_CA: 1.
PROSITE: PS01187: EGF_CA: 1.
PROSITE: PS01241: LINK: 2.
PROSITE: PS01241: LINK: 2.
PROSITE: PS01615: C_TYPE_LECTIN_1: 1
PROSITE: PS00141: C_TYPE_LECTIN_2: 1.
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SIGNAL
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DOMAIN
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Signal; Repeat; EGF-like domain; Calc
Hyaluronic acid; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART: SM00409; IG; 1
SMART: SM00445; LINK:
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SMART; SM00001; EGF_like;
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2 KEYFTS 7
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293
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                                                                             88.98;
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                                                  W-LINKED (GLONAC. ...) (P
N-LINKED (GLONAC. ...) (P
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                                   Score 32:
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N-LINKED (GLCNAC
N-LINKED (GLCNAC
N-LINKED (GLCNAC
N-LINKED (GLCNAC
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EGF-LIKE 2. CA
C-TYPF LECTIN.
SUSHI
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N-LINKED (GLONAC:
N-LINKED (GLONAC:
N-LIDKED (GLONAC:
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                          Pred No.
                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COPF PROTEIN.
V-TYPE DOMAIN.
                                   DB 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                     CALCIUM-BINDING (POTENTIAL).
                            1.7e+02;
                                   Length 3562;
                   Indels
                                                      CPC64;
                                                                                     (POTENTIAL)
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                                                                     (POTENTIAL)
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                   Gaps
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TC1_DICOL

TC1_DICOL

C 015746

TC 015746

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ENULT 4

15'9_YEAST STANDARD: PRT: 1460 AA.
D N15'9_YEAST STANDARD: PRT: 1460 AA.
C P40477;
T 01-FEB-1995 (Rel. 31, Created)
T 16-0CT-2001 (Rel. 40, Last annotation update)
T 16-0CT-2001 (Rel. 40, Last annotation update)
N NCP159 OF RAT7 OR YILLISO.
N NUP159 OF RAT7 OR YILLISO.
S Saccharomyces cereviside (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 86.1%:
Best Local Similarity 85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright, it is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMRL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as income as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a libers attemptor (see http://www.isbbsib.chbanc.com/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOOMIS W.E. TYARFAY N.

Submitted (AUS-1997) to the EMBL/GenBank/DDRT databases
-i- EUNCTION: CATALYZES THE CONVERSION OF 3%-PHOSPHARE TO A 2%,3%-
CYCLIC PHOSPHODIESTER AT THE END OF RNA. THE MECHANISM OF ACTION
OF THE ENZYME OCCURS IN 3 STEPS: (A) ADENYLATION OF THE ENZYME BY
ATP; (B) THE ENZYME ACTS ON RNA.N3%-P TO PRODUCE RNA-93%-PAS%-(C)
A NON CATALYTIC NUCLEOPHTIC ATTACK BY THE ADJACENT 2*HYLMOXYL ON
THE PHOSPHORUS IN THE DIESTEP LINKAGE TO PROCUCE THE CYCLIC END
PRODUCT THE BIOLOGICAL POLE OF THIS ENZYME IS ONKOMEN BUT IT IS
LIKELY TO FUNCTION IN SOME ASPECTS OF CELLULAR PNA PROCESSING (BY
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   015746;
15-DEC-1998 (Rel 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable RNA 3'-terminal phosphate cyclase (EC 6.5 1 4) (PNA-3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF020279; AAB70847.1; -. DictyDb: DD0????; -.
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Eukaryona: Mygetozwa, Clotywstellida; Flotywstelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ligase: Nuclear protein.

ACT_SITE 354 354

SEQUENCE 433 AA: 47110 MW:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 IKSYFTS 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: ATP + RNA 3'-terminal-phosphate - AMP + diphosphate + RNA terminal-2',3'-cyclic-phosphate. 1 diphosphate + RNA terminal-2',3'-cyclic-phosphate. 1 diphosphate + RNA terminal-2',3'-cyclic-phosphate. 1 diphosphate + RNA terminal Gyclasm (By similarity). SIMILARITY: RELONGS TO THE RNA 3'-TERMINAL CYCLASE FAMILY. SUBFAMILY 1. CAUTION: THE C-TERMINAL SECTION OF THIS PROTEIN COULD BE INCORPRETED AND THE REAL PROTEIN IS PROBABLY SHORTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _DICDI
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Pred. No. 30;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F3AFFBC044458CE9 CBC64;
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Query Match
Best Local Similarity
Thickes 5. Conserve
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                                      PTKA_ECOLI STANDAPD: PRT: 150 AA.

P37187; P76413;
01-0CT-1994 (Rel. 30, Created)
01-NCV-1997 (Rel. 35, Last sequence spokete)
15.JUN-2022 (Rel. 41, Last innotation update)
PTS system, galactitud-Specific IIA component (EliA-GAT) (Galacticol-permease IIA component) (Phosphotransforage enzyme II A component)
(EC 2.7.1.69).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barrell BG. Badcock K. Bankler A T. Bowman S. Brown D. Ghurcher C.M., Connor R., Copsey T. Pear S. Devlin K., Fraser A., Centres S., Hamlyn N., Borsnell T.S., Rint S., Jayels K., Jones M., Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D., Bajandream M.A., Piles L., Rowley N., Skelton J., Smith V., Whitehead S., Submitted (EPP-1444) to The EMBLANA AND DEBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                Nuclear protein; Transport; Repeat LOWMAIN 518 617 4 X 27 AA TANDEM REPEATS. REPEAT 518 543 1. REPEAT 544 569 2. REPEAT 570 595 3.
                                                                                                                                                                                                                                                               1190 LKEYYTS 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gorsch L.C., Dockendorff T.C., Cole P.N.;
"A conditional allele of the novel repeat-containing yeast nucleoporin RATT/NUP159 causes both rapid cessation of mRNA exportant reversible clustering of nuclear pore complexes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=95263675; PubMed=7744966;
Gorsch L C , Dockendorff T C , Co
Escherichia coli, and Escherichia coli 0157:H7
                                 GATA OR B2094 OR Z3257 OR ECS2897
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL: L40634: AAC41652 1; -.
EMBL: 738125: CAA86265.1; -.
PIR: S48457: S48457.
SGD: S0001377: NUPLS9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib-ch/announce/or send an email to license@isb-sib-ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright it is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- DOMAIN: CONTAINS A CENTRAL REGION WITH REPEATS THAT ARE X-X-F-G, PRIMARILY S-A-F-G AND P-S-F-G, NOME OF THESE REPEATS ARE EMBEDDED WITH IN 3 NEARLY PERFECT 26 AMINO ACID TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes, Saccharomycetales, Saccharomycetae.... Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell Biol. 129:939-955(1995).
                                                                                                                                                                                                                                                                                              1 IKEYFTS 7
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570 5
596 6
1460 AA;
                                                                                                                                                                                                                                                                                                                                   Conservative
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71 4%;
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STRAIN-0157:H7 / RIMD 0509952;

MEDLIND-2115623]; PLUMEd-1128776;

Hayashi T., Makiho K., Ohnishi M., Kurukawa K., Ishii K., Yukuyama K.,

Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Tida T., Takami H., Honda T., Sasakawa C., Oqusawara N., Yasunaga T.,

Kuhara S., Shiba T., Hatturi M., Shinagawa H.,

Complete genome sequence of enterchemorphagic Escherichia coli

Ol57:H7 and genomic comparison with a laboratory strain K-12.*;

NA Pac R. 11-22-7601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nobelmann B., Lengeler J.W.; "Sequence of the gat operon for galactitol utilization from a wild-type strain EC3132 of Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perna N.T., Piunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Grogor T., Kikkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria: Proteobacteria:
Escherichia:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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MEDLINE-21074945: PubMed-11205551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 277:1453-1474(1997).
                                                                                                              EcoGene; EG12414; gatA.
InterPro; IPR002178; PTS_EIIA_2
                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb/sib/ch/ammonner/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL cutstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of enterchaemorrhagic Escherichia coli 0157.H7.":
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license isb sib.ch).
Phosphotransferase system: Sugar transport: Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENDLPYBUVATE-DEPENDENT SUGAR PHOSPHOTPANSFERACE SYSTEM (PTS). A MAJOR CARBOHYDRATE ACTIVE SUGAR PHOSPHOTPANSFERACE SYSTEM (PTS). THE STAND THE STARD THE SYSTEM. THE STORE SHOULD SITE AND THE TRANSMEMBRANE CHANNEL: THE STA DOMAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DOWN'S SPHOTHER). ITA STANSFERS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         histidine + sugar phosphate.
SUBCELLULAR LUCATION: Cytoplasmic.
SIMILARITY: CONTAINS 1 PTS EIIA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: Protein N-phosphohistidine + sugar * protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
                                                                                                                                                                                      X79837; CAA56228.1; -. AE000298; AAC75155.1; -. AE005435; AAC57151.1; -. AP002560; BAB46420 1; -
                                  pF00359; pTS_EIIA_2; 1.
m; pD001689; pTS_EIIA_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8:11-22(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blophys. Acta 1262.69 72(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gamma subdivision, Enterobacteriaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Yokoyama K.,
Tobe T.,
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PYBL_PEA STANDARD: PRT: (05 AA. DYBL_PEA STANDARD: PRT: (05 AA. AC 043086: DT 15-DEC-1998 (Rel. 37, Created) DT 15-DEC-1998 (Rel. 37, Last sequence update) DT 15-DEC-1998 (Rel. 37, Last sequence update) DE 15-DEC-1998 (Rel. 41, Last sequence update) DE Aspartate carbamoyltransferase 1, Chigroflast procursor (EC 2.1.4.2)
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                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Physiol. 105:377-384(1994).

-!- CATALYTIC ACTIVITY: Carbamoyl prosphate + L-aspartate -

-!- N-carbamoyl-L-aspartate.

-!- ENYME REGULATION: ALLOSTERICALLY REGULATED BY UMP.

-!- PATHWAY: Pyrimidine biosynthesi: second step.

-!- SUBUNIT: HOMOTELMER (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyla: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta; eudicolyledons; core eudicots: Rosidae: eurosids I, Eddales, Fabaceae, Papilionolideae; Viclede) Pisum.
                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see hit; ...www.lsb-sit-dlouble-deep or send an email to license@isb-sib-th).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-cv. Wando; TISSUE-Leaf;
MEDLINE-94402175; PubMed-8029359;
Williamson C.L., Slocum R.D.;
                                                                                                                                                                                                                                                                                    InterPro: IPR002029: Asp_Orn_Cotract.
InterPro: IPR002082; Asp_carbmltransf.
pfam; PF00185; OTCace; 1.
pfam; PF02729; OTCace_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular cloning and characterization of the pyrBl and pyrB2 genes
encoding aspartate transcarbamoylase in pea (Pisum sativum L.).";
Plant Physiol. 105:377-384(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pisum satiwum (Garden pea)
                                                                                                                                             SEQUENCE
                                                                                                                                                                                                 Multigene family.
                                                                                                                                                                                                                                    TIGREAMS; TIGRO0670; asp_carb_tr: 1
PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
                                                                                                                                                                                                                                                                                                                                                                  EMBL; M96981; AAA62443.1; HSSP; P00479; GCSU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on the law that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197 IMEYET 142
                                                                                                                                                                                TRANSIT
                                                                                                                                                                                                                    Pyrimidine biosynthesis; Transferase; Chloroplast; Transit peptide;
                                                                                                                                                                                                                                                                         PRINTS; PROCIDO: ACTUASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Aspartate transcarbamylase 1) (ATCuse 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
 275 IKEYLTS 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IKEYFT 6
                                1 IKEYFTS 7
                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  non-profit institutions as long as its content
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                                                                                                                                             386 AA;
                                                                     Conservative
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83.3*;
                                                                                                                                           386 ASPARCATE CARBAMOYLTRANSFERASE 42617 MW, A9440F45474E29F4 CRC64;
                                                                                         83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                     Score (1); DB
Pred. No. 44;
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                                                                       Mismatches
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                                                                                                            DB 1:
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                                                                                                          Length 386;
                                                                         Indels
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ANB_PIRSP
D MANB_P
C P55297
T 01-0CT
T 01-0CT
T 15-JUL
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ANC_PIRSP
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SIGNAL
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01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Mannan endo-1,4-beta-mannosidase Crecursor
01-OCT-1996 (Rel. 34. Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Mannan endo 1,4 beta-mannosidase B predursor (EC 3.2.1.78) (Beta-
                                                                                                                                                                                                                                                                                                                            REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                        CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arose through gene duplication.

FEMS Microbiol. Lett. 141:183-188(1996).

-!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-beta-D-mannesidic linkages in mannans, galactomannans, glucomannans, and galactoglucomannans.

-!- SIMILARITY: THE 39 AA REPEATS ARE SIMILAR TO THOSE IN MANA, MANC AND XYNA, AND TO THOSE OF N. PATRICIARUM XYNA.
                                                P55297;
01-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro: IPR002883; CBD_5.
Interpro: IPR000805; Glyco_hydro_26.
Interpro: IPR001230; Prenyl_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities regulies a license agreement (See http://www.isb-sib-ch/announce, or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=96313314; PubMed=8768520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neocallimasticaceae: Piromyces. NCBI_TaxID=45796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mannanase C) (1,4-beta-D-mannan mannanohydrolase C).
                                                                                MANB_PIRSP
                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00739; GLHYDRLASE26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X97520; CAA66134 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bloinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Piromyces sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P55298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO FAMILY 26 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Evidence that the Piromyces gene family enceding ender1,4-mannanases
                                                                                                                                                        444 LKEYET 449
                                                                                                                                                                                                                                 Local similarity
                                                                                                                                                                                     1 IKEYFT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                               PF02013; CBM_10; 2.
PF02156; Glyco_hydro_26; 1.
                                                                                                                                                                                                                                                                                480
569
                                                                                                                                                                                                                                                                                                                                                                                      Glycosidase: Signal: Multigene family: Repeat.
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                                                                                 STANDARD;
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477
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                                                                                                                                                                                                                                                                                64115 MW;
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                                                                                                                                                                                                                                 Score 30; DB
                                                                                                                                                                                                                                                                                POLY-ASN.
; 19277764E18328B5 CRC64;
                                                                                                                                                                                                                                                                                                              POLY-ASN
                                                                                                                                                                                                                                                                                                                                                        MANNAN ENDO-1,4-BETA-MANNOSIDASE C 2 X 39 AA APPROXIMATE REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT:
                                                                                                                                                                                                                 Mismatches
                                                                                571 AA
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PRESENTATION OF THE PRESEN
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Best Local
                                                                                                                                                                                                                                                         01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 27.1 kDa protein UED4 (API inter
YKL009W OR YKL160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                             Eukaryota; Fungi; Ascomycota, Saccharomycotina; Saccharomycetes Saccharomycetales; Saccharomycetacoae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                 YKA9_YEAST
P33201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib-ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96313314; PubMed=8768520; Millward-Sadler S.J., Hall J., Plank J.W., Hazlewood G.P.,
Pascolo S., Ghazvini M., Boyer J., Colleaux L., T
"The sequence of a 9.3 kb Segment coated on the
                                                         MEDLINE=93127732; PubMed=1481574;
                                                                                                                                                                          Saccharomycetales;
                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (out http://www.ish.vilt.ch/annenter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neocallimasticaceae; Piromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;
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                                                                                        SEQUENCE FROM N.A.
                                                                                                                                              NCBI_TaxID=4932;
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InterPro: IPR002883: Alymo_bydro_2/
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SIMILARITY: BELONGS TO FAMILY 26 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                galactoglucomannans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF02013; CBM_10; 2.
PF02156; Glyco_hydro_26; 1.
S; PR00739; GLHYDPLASE26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-ASN.
; B13F44581FAA9DAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MANNAH ENDO-1,4-BETA-MANNOSIDASE B. 2 X 34 AA APPROXIMATE REPEATS.
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                                 Dujon B.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          yeast chromosome XI reveals five open reading frames including the CCE1 gene and putative products related to MYO2 and to the ribusomal protein L10.
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Yeast 9:279-287(1993
                                                                                                                                                                     Nelson K.E. Clayton R.A. Gill S.R. Gwinn M.L. Dodson R.J., Hart D.H., Hickey E.K., Peterson J.D., Nelson W.C. Ketchum K.A., McDonald L. Utterback T. P. Majek J.A. Linher K.D. Garrett M.M., Stewart A.H., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O., Salzberg S.L., Smith H.C., Venter J.C., Eraser C.M., Salzberg S.L., Smith H.C., Venter J.C., Eraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           i0-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
Heat-inducible transcription repressor hack homological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib-sh/announ-eoor send an email to licensevisb-sib.ch).
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               genome sequence of Thermotoga maritima.":
Nature 399:323-329(1999).
-i- FUNCTION: NEGATIVE REGULATOR OF CLASS I HEAT SHOCK GENES (GRPE-DNAK-DNAJ AND GROELS OPERONS). PREVENTS HEAT-SHOCK INDUCTION OF THESE OPERONS (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-MSB8 / DSM 3109;
MEDLINE-99287316; PubMed-10360571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermotoga maritima.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barteria; Thermotogae; Thermotogae
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-!- SIMILARITY: BELONGS
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les 5, Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00466: Ribosomal_L10.
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Pred. No.
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HRCA FAMILY
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PPCT entry is copyright it is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                            "The AcbC protein from Actinoplanes species is a C7-cyclitol synthase related to 3-dehydroquinate synthases and is involved in the biosynthesis of the alpha-glucosidase inhibitor avarhose.";
J. Biol. Chem. 274:1089-10896(199")
J. Biol. Chem. 274:1089-10896(199")
J. Biol. Chem. C7-cyclitol synthase using sedo-heptulose 7-phosphate, but not ido-heptulose 7-phosphate and 3-deoxy-arabino-heptulosonate 7-phosphate, as a substrate. Involved in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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TIGPFAMS; TIGR00331: hrcA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE001751; AAD35933.1; ...
                                                                                              the European Bioinformatics Institute. There are no restrictions on modified and this statement is not removed. Usage by and for commercentities requires a figures agreement that the http://www.isbosil.blooms.com.send.an.email.to.license@isbosib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Fel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-yun-2002 (Rel. 41, Last annotation update)
2-epi-5-epi-valiolone synthase (EC 4.2.3.-) (Sedo-heptulose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACBC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGR; TM0851
                           InterPro: IPR002658; DHQ_synthase. Pfam; PF01761; DHQ_synthase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Actinobacteria; Actinobacteridae; Actinobacteridae; Actinomycetales; Micromonosporineae: Micromonosporaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphate cyclase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9ZAE9;
                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bivintormatics and the EMBL outstation .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Piepersberg W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stratmann A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-99214159; PubMed-10196166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actinoplanes sp. (strain 50/110)
                                                                  EMBL; Y18523; CAA77208.1; 1.
                                                                                                                                                                                                                                          -!- COFACTOR: NAD and a divalent motal cation such as cobalt.
              Lyase; NAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                328 LSEYFTS 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IKEYFTS 7
                                                                                                                                                                                                                                                                                              inhibitor acarbose.
CATALYTIC ACTIVITY: Sedo-heptul se 7-phosphate • 2-opi-5-opi-
                                                                                                                                                                                                                                                                              valiolone +
                                                                                                                                                                                                                                                                                                                                 biosynthesis of the acarviose wellety of the alpha-glucosidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR002571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       338 AA;
382 AA; 42181 MW; EDA, POGGA, 14PARA TRO64.
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            Cobalt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mahmud T., Lee S., Distler J., Floss H.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                               phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39306 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HrcA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       esso: Heat shock, Compl
02A5/5A546C313AE (RC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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ESULT 12
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                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a livense agreement (See http://www.isb.sib.ch/annimic.or send an email to license@isb-sib.ch).
                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics, and the EMBL outstation
                                                                                                                                                                                                                                                                                                       EMBL; Z99120; CAB15258.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Probable cysteine desulfurase (EC 4.4.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98044033; PubMed-9384377;
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nes 5: Conserv
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                                                                                                                                                                                                                                                     COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEVENDENT
                                                                                                                                                                                                                                 AMINOTRANSFERASES CSD SUBFAMILY
                                                                                                                                                                                                                                                                                                    ATOMS FROM I-CYSTEINE, L-CYSTINE, L-SELENOCYSTEINE, SELENOCYSTINE TO PRODUCE L-ALANINE (BY SIMILARITY).
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Pred No.
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Best Local
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010127;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
10-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical zinc finger protein FG-9.1 in chromosome II.
F56D1.1.
                                                                                                          SEQUENCE
                                                                                                                                                                                                                                 PRINTS, PROCO48, ZINCPINGER.

SMART, SHOCUSE, CHP_COHO; 5.

PROSITE: PSS0157: ZINC_FINGER_C2H2_1; 3.

PROSITE: PSS0157: ZINC_FINGER_C2H2_1; 4.
                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sip.ch).
                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions of long as its content is in no modified and this statement is not concerd. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam: PF00266; aminotran_5; 1. PROSITE; PS00595; AA_TRANSFER_CLAS: _5: 1.
                                                                                                                                                                                                                                                                                                                                EMBL; U39997; AAA81101.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (NOV 1935) to the EMBL, Diseast, EERI databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fukaryota: Metazoa: Nematoda: Chromilorea: Rhabditida: Rhabditoideu:
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                                                                                                                                                                                                       Hypothetical protein; Zinc-finger; HNA-binding; Metal-binding; Nuclear protein; Repeat.
                                                                                                                                                                                                                                                                                           Pfam; PF00095
                                                                                                                                                                                                                                                                                                     calaster
                                                                                                                                                                                                                                                                                                                   WormPep; F56D1.1; CE01969.
                                                                                                                                                                                                                                                                                                                                                                         entities regulies a license agreement (See http://www.isb-sib-shyanmanner
                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Nuclear (Fotential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chissoe S., Wilson R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhabditidae: Peloderinae: Caenorha: titis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000192; AminotransfV.
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150 IKEYHTS 156
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                           1 IKEYFTS ?
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es 5; Conserv
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G 224 PYRID: NAL PHOSPHATE (BY SIMILARITY).

CE 406 AA: 44922 MW: E43: 0B5965349Dl CRC64;
                                                    Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                          SS-FROT entry is copyright It is produced through a collaboration the SWISS Institute of Bildrormatics and the EMBL outstation.
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                                                                                                                                   46
73
103
130
317
                                                      Conservative
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                                                                                                                                                                                                                                                                                        zf-C2H2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                       68
126
154
154
340
                                                                                                          50097 MW;
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H2: 5.
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83.3%;
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Pred, No.
                                                                  Score 19; DE
Pred. No. 81;
                                                                                                                      C2H2-TYPE
                                                                                                                                                                                           C2H2-TYPE.
                                                                                                          2400A 495F75343D6 CRC64;
                                                      Mismatches
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SULT 15
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Excinculease ABC subunit C.
UVRC OR CPE0352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Flesh-eater.":

Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).

Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).

Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).

PROC. Natl. THE ABC EXCISION NUCLEASE IS A DNA REPAIR ENZYME THAT CATALYZES THE EXCISION REACTION OF UV-DAMAGED NUCLEOTIDE SEGMENTS PRODUCING OLIGOMERS HAVING THE MODIFIED BASE(S). ATTACHES TO THE UVRA-UVRB COMPLEX, DISPLACING UVRA, AND THE DAMAGED NA STRAND IS NICKED ON BOTH SIDES OF THE DAMAGED SITE (BY SIMILARITY).

PRODUCT: Consists of three subunits; uvra, uvrB and uvrc.

PROBLELLULAP LOCATION: Cytoplismic (By Similarity)

PROBLELLULAP LOCATION: Cytoplismic (By Similarity)

PROBLELLULAP CONTAINS 1 UVP DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UVRC_CLOPE 08XNI1;
004781; Q04029;

01-NDV-1997 (Rel. 35, Created)

01-NDV-1997 (Rel. 35, Last sequence update)

16-0CT-2001 (Rel. 40, Last annotation update)

Hypothetical 180.2 kDa protein in FAA4-HOR7 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb/slb/dimounce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium perfringens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOS response; Excision nuclease; DNA repair; Complete proteome DOMAIN 204 239 UVR. SEQUENCE 620 AA; 71390 MW; 6E04ADE9C3849Z19 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART: SM00465; GIYC: 1.
TIGREAMS: TIGR00194; uvrC: 1.
PROSITE: PS50151: UVR: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                   YM81_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01541; Exci_endo_N; 1. Pfam; PF02151; UVR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro: IPR001943; UVrB/C.
InterPro: IPR004791: UVrC.
InterPro: IPR001162; UVrC_C.
InterPro: IPR000N05: UVrC_N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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PubMed-11792842;
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71.4%;
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Pred. No. 1.2e+02;
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Search completed: April 8, 2003, 12:02:17
Job time : 19.9167 secs
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gentles S., Bowman S., Barrell B.G., Rajandream M.A., Wa
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-!- SIMILARITY: STPONG, TO HUMAN ZNE294.
                                                                                                                                                                                                                                   PROSITE: PS00518; ZF_RING_1; FALSE_NFG.
PROSITE: PS50089; ZE_RING_2; 1.
Hypothetical protein: Zinc-finger.
ZN_FING 1508 1555 RING-TYFE.
                                                                                                                                                                                                                                                                                                        EMEL: 248639; CAAR8574.1; -.
EMBL: 248756; CAA88657.1; -.
SGD: SQN04861; YMP247C.
ThterPro: (FB00184; Znf_ring.
SMART: SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hunt S., Bowman S., Barrell B.G., Rajandream M.A., Walsh S.V.; Submitted (MAR-1995) to the EMBL/GenHank/DDBJ databases.
                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=S288c / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 950-1562 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-955 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YMR247C OR YM9408.09C OR YM9920.01C
                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch)
                                                                        462 IEDYFTS 468
                                                                                                                                             Local Similarity nes 5; Conserv
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                                                                                                                                                               80 68; Score 34
71.48; Pred. No.
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GenCore version 5.1.4\_p5\_4578

Copyright (a) 129 : 2003 Compages End.

M protein : protein search, using sw model

un on: April 8, 2003, 11:59:15; Search time 30.9167 Seconds (without alignments)
21 766 Million cell updates/secoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
earched: 283224 seqs, 96134422 residues

2: plr2:\*
3: plr3:\*
4: pir4:\*

ost-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries otal number of hits satisfying chosen parameters.

283224

Inimum DB seg length: 0
aximum DB seg length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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# ALIGNMENTS

T32922 T32921 T32922 T32922  Pypothetical protein K09H9.5 - Caenorhal-ditis elegans C)Species: Caenorhabditis elegans C)Species: T32922 R)Madsen, C) Graves, T.; Blair, T. Submitted to the EMBL Data Library, January 1998 R)Madsen C) Graves, T.; Blair, T. R)Madsen C) Graves, T. R)Madsen C) Graves, T.; Blair, T. R)Madsen C) Graves,	Query Match 88.9%; Score (2: DB 2: Length 278: Rest Local Similarity 100 0% Pred No. 29: Matches 6: Conservative 0: Missautches 0: Indels 0: Caps Oy 1 IKEYFT 6	RESULT 1  BY TABLE 1. Thermotoga maritima (st c)species: Thermotoga (st c)species
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Katsoulou, ast 12, 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bmitted to the EMBL Data Library, May 1995
Description: The complete sequence of a 40.7 kb segment located on the left arm of year east hypothetical proteins.
Reference number: S55159
Accession: S55167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Saccharomyces cerevisiae
Date: 08-301-1995 *sequence_revision 01-Sep-1995 *text_chingo 21-301-2000
Accession: S55167: S55718: S56928; S71651
Xatsonlon: C - Tzermia M - Alexandraki D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Sus scrofa domestica (domestic pig)
Date: 04-Decriss *sequence_revision of Decribs * fext_change is contible
                                                                                                                                               Molecule type, DNA Residues: 1-268, F. 269-281, F. 284-460, W., 762-460 ASIA Residues: 1-268, F. 269-281, F. 284-460, W., 762-460 ASIA Cross-refarences EMBL H21726, NID.; 885973, FID g885974 Katsoulou, C.) Tzermia, M.; Alexandraki, D. bmitted to the Protein Sequence Database, September 1995 before number, 856912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E2-dependent signaling protein - yeast (Sacobaromyces cerevisiae)
Alternate names: protein J0642; protein YJL146w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Experimental source, submandibular gland
Keywords: 2Fe·2S; cytosol: Iron·sulfur protein: monomer; NAD, oxidoreductase
53-58,389-395/Region: Iron binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                      Sia, R.A.; Mitchell, A.P.
bmitted to the EMBL Data Library, February 1995
Description. A novel gene, IDS2, is required for IME2-dependent functions.
Reference number: S55718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: EMBL:X87371; NID:g854542; PID:g854551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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186-206/Region: cytochrome b5 binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: mRNA
Residues: 1-415 <SCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-N-acetylneuraminate monooxygenase (EC 1.14.13.45) - pig (fragment)
                                                Cross-references: EMBL:249421: NID:gl015558: PID:gl015559; MIPS:YJL146w
                                                                          Molecule type: DNA
Residues: 1-469 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: DNA
Residues: 1-469 <KAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession: S68831
                                                                                                                                    Accession: S56928
                                                                                                                                                                                                                                                                                                                               Accession: S55718
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                       Tzermia, M.; Tavernarakis, N.; Alexandraki,
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R:Chambaud, I.; Hoilig, R.; Ferris, S.; Parbe, V.; Samson, D.; Galisson, F.; Moszer, Rucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma A;Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dμ
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A:Title: Molecular cloning of cytidine manaphaspho-N-acetylneuraminic acid hydroxylas A:Reference number: A57469, MOID:9533231.2. PMID:7608218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CMF-N-acetylneuraminate monooxygenase (ECL) 14.13.45) - mouse NyAlternate names: CMF-NeuAc hydroxylase) cytidine monophosphe-N-acetylneuraminic aci C/Species: Mus musculus (house mouse) C/Species: Mus musculus (house mouse) C/Date, 08-Dec-1995 #sequence_revision -08-Dec-1995 #text_change 05-Nov-1999
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A; Residues: 1-469 < K
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A;Accession: S71651
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                                                                                                                                                                                                                                                                                                                                                                                                  lipoprotein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: E90575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              γÇ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Description. This is the key emzyme for the synthesis of R\text{-}\mathrm{glycolyl}\mathrm{neuraminic} acid G:Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-577 < KAW>
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A; Status: preliminar
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                                                A; Genetic code: SGC3
                                                                          A; Gene: MYPU_5090
                                                                                                                             A; Experimental source: strain UAB CTIP
                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-620 < KI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Residues: 1-577 <
A:Cross references
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: A57469
                                                                                                                                                             A;Cross-references: GB:AL445566; PID:gl4:089423; PIDN:CAC13682 1: GSPDK:GN00153
                                                                                                                                                                                                                                          A;Status: preliminary
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.2 1.33.3.3.1 2.75
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6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IKFYFT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary; not compared with conceptual translation
                                                                                                                                                                                    1-620 <KUR>
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Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB-D21826; NID-g927-54: PIDN-BAA04850.1; PID:d1005385: PID:g92765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 9%; Score
  88.98;
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  Score 12;
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                                                                                                                                                                                                                                                                                                                                                                              S.; Parbe, V.; Samson, D.; Galisson, F.; Moszer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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49;
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  2: Length 620
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ESULT 9
51225
naill protein - zebra fish
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hondroitin sulfate proteoglycan PG-M core protein - chicken; Species: Gallus gallus (chicken); Date: 21-Sep-1993 *sequence_revision 18-Nov-1994 *text_change 21-Jul-2000; Accession: A47171; Shinomura, T.; Nishida, Y.; Ito, K.; Kimata, K.; Bioi. Chem. 258, 14451-14459, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :Hammerschmidt, M.; Nusslein-Volhard, C. evelopment 119, 1107-1118, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superfamily: chicken should with sulfate probegly an PS-M some protein. Crype leads: 1166-243, Domain. Link protein repeat bomology sunki.
264-345, Commain. Link protein repeat bomology sunki.
33198-325, Commain. ESF hourings such.
33198-325, Commain. ESF hourings such.
3329-3327, Commain. ESF hourings such.
3339-3327, Commain. Crype leads homology such.
3349-3457, Commain. Crype leads homology such.
                                                                                                                                                                                                                                                                                                                                                                                                                                       :Status: preliminary, translated from GB/EMBL/5565;
Molecule type. mRNA
;Residues: 1-260 <HAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: I50109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :Title: The expression of a rebrafish gene homologous to Drosophila small suggests:Reference number: I50109: MUID:94139555; PMID:8306877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: GB:D13542: NID:g391643; FIDH:BAA02742.1; PID:g391644; Experimental source: stage 22-23 developing limb buds; NCBIP:134457); Note: sequence extracted from NCBI backbone (NCBIN:134456, NCBIP:134457)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Status: preliminary
;Molecule type: nucleic acid
;Residues; 1-3562 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :Title: cDNA cloning of PG-M, a large chandroitin sulfate protenglycan expressed during
                                                                                                                                                                                                                                                                                                                                                          :Gene: sna-l
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                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: EMBL:X74790; NID:4468620; PID:4468621
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                                                                                                                                      VKKYFTS 13
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                                                                                                                                                                                                                                                                          86.18;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.78
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1: Mismatches
                                                                                                                                                                                                                                                                       Score 31; DB
Pred. No. 44;
                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                   DB 2; Length 260;
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A:Molecule type: DNA
A:Residues: 1-1460 <BOWS
A:Residues: 1-1460 <BOWS
A:Residues: 1-1460 <BOWS
A:Residues: GR 747647, EMBC 238:,5 NID y603997, FTD.y763231, MIDC.YIEllSo P:Gorsoh, L C : Dookendorff, T C , Cole G.N.
J. Cell Biol 129, 939-955, 1995
A:Title: A conditional allele of the social repeat-containing yeast sucleoperin PAT7
A:Peference number: A57285; MUID-95263675: PMID-7744466
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S48457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C)Function:
A Description involear para complex protein involved in mRNA export C;Keywords: nucleus
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submitted by the EMET Cata (throry
A:Reference number: S48455
A:Accession: S48457
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C:Date: 13-Sep-1996 #sequence_revision | 5-Sep-1996 #text_change 31-Jan-1997
C:Accession: I51225
                                                                                               C:Species: Escherichia coli
A:Variety: strain EC3132
C:Date: 28-Oct-1995 #sequence_revision | Nove-1995 #fext_change OB-Oct-1999
                                                                                                                                                                                                                                                                                                                  В
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A:Residues: 1-1101, T, 1103-1460 <00P:
A:Cross-references: GB:L40634
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K.Alturnate names: protein YIL115c
C.St. Nice Cosciety - D
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C;Genetics:
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                   R:Nobelmann, B.; Lengeler, J.W. Biochim. Biophys. Acta 1262, 69-72, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
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A; Residues: 1-263 <THI>
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A;Status: preliminary; translated from GH/EMBL/DDBJ
A;Title: Sequence of the gat operon for galactitol utilization from a wild-type strai
                                                                      C; Accession: S55903; S49081
                                                                                                                                                                              phosphotransferase system enzyme II,
                                                                                                                                                                                                                                      RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: SGD:S0001377; MIPS:Y;L115c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A57285
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Pares: Objects 1994 #sequesor_foolsis: 
Accession: 8484sm; Asize85
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                     1190 LKEYYTS 1196
                                                                                                                                                                                                                                                                                                                                                                                                                             local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score (1) DB 2;
Pred. No. 2.6e+02;
2; Mismatches ()
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Pred. No. 45;
2: Mismatches 0: Indels
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В

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IA Res. 8, 11-22, 2001
Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genome Reference number: A99629; MUID:21156231; PMID:11288796
Accession: A90991
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Residues: 1-150 ≺NCB→
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s system, Julactitul-specific IIA component - Escherichia coli (strain 0157:H7, substr
Species: Escherichia coli
Date: 18-Jul-2001 *sequence_revision 18-Jul-2001 *text_change 27-Mon 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: GB:AE000298; GB-000096; NID:g1786395; FIDN:AAC75155.1; FID:g1788410.
Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cq.; Rose, D.J.; Mau, B.; Shao, Y.
ience 277, 1453-1462, 1997
Title: The complete genome sequence of Escherichia coli K-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: E64976
Status: preliminary: nucleic acid sequence not shown: translation not shown
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                                                                                                                                                                                                          Cross-references: GB:BAᲔᲛᲔᲛᲔᲛ?; PIDN BAB36320.1: PID:gl3362366; GSPDB:GNOG154
Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, sawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: A90991
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                                                                  Matches
                                                                                                                                                             Gene: ECs2897
                                                                                                                                                                                                                                                           Molecule type: DNA
Residues: 1-150 <HAY>
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    Mismatches

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C;Date: 16 Feb.2001 #Sequence_revision: 1/ Feb.2001 #text_change 27 How 2001 C:Accession: C88836
R.Perna, N.T., Flunkett III, G.; Burland V.; Mau, B.; Glasner, J.D.; Rose, D.J.; iller, L.; Grotbeck E.T.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W.Alternate names aspartate transcarbon-ylase c:Species: Triticum aestivum (common wheat) c:Date: 19-Mar-1997 #sequence_revision .54-Aug-1997 #text_change 07-May-1999 c:Accession: S47625 R.Bartlett, T.J.; Aibangbee, A.; Bruce, I.J.; Donovan, P.J.; Yon, R.J. Biochim. Biochim. 1207, 187-193, 1994 A.Title: Endogenous polypeptide-chain length and partial sequence of aspartate transca. A.Reference number: S47625; MUID:943553'4: PMID:8075153 A.Recession: S47625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-150 <570>
A;Cross-references. GB.AE005174; NID:q1:015297; PIDN:AAG57151.1: GSPDB GN00145; UWGP:
A;Experimental source: Strain O157:H7, sobstrain EDL933
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Reference number: A85480; MUID:2107493%; PMID:11206551
A:Accession: C85836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Escherichia coli
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                                                                                                                                                                                                                                                                                                        A:Experimental source: var. Avalon C:Superfamily, ornithine carbamoyltrans(crase: asparta*e/ornithine carbamoyltrans(crase: homotrimer C:Keywords: pyrimidine nucleotide biosynthesis: transferase: homotrimer F:1-223, Comain. aspartate/ornithine carbamoyltransferase homology (tranment) <ACT>
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Job time .
                   Search completed. April
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

esult No	score	Match Query	Query Match Length DB	E.G.	IP.	Description
<u>.</u>	30	8 . 12 . 12 . 12 . 1	150	10	rs-09-741-669-424	Sequence 424, App
t i	29	े हे. के	55.63	5	#8-09-815-242-12610	
ų.	e G	7 7	141	=	08-09-815-646-11689	Sequence 11289, A
4	28	77.8	141	10	US-09-815-242-11471	
л	28	77.8	219	10	115-09-782-874-3	
6	e a	ם ווו	13 A	.5	PS-09-912-020-350	Sequence 350, App
7	28	77 9	276	12	115-10-033-078-16	
8	ല	77.8	377	10	US-09-910-430-27	Sequence 27, Appl
9	28	77.8	431	9	US-10-081-816-5	Sequence 5, Appli
16	r.,	17 X	5.1.	r	118-04-7 km-626-5505	Sequence Saus, Ap
11	28	-1 -1 -0	(n (-)	5	US-09-815-242-10760	Sequence 19760 A
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13	ca a	11 0	121	. <u>.</u>	ms-na-815-242-50a3	Sequence sous, Ap
14	(4 Q)	77.8	1114	3	#E-09-782-874-2	Sequence 2, Appli
15	27	75.0	<u>بر</u> 22	10	US-09·144·838·14	Sequence 14, Appl
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17	27	35.0	نیا	10	US-09-144-838-15	Sequence 15, Appl
18	27	ш ,л ,	34	10	US-09-144-838-16	Sequence 16, Appl
19	27	35.0	in	17	US-10-001-870-147	Sequence 147, AFF

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US-107-275-8	09-08-12-939-21	77-	US-09: 144-838-45	144-838-	195-4	- 1	144-838-4	144 939	144-8	US-09 144 838-34	.144	1	US-09:864-761-40180	•	144-838-4	144-838-3	144-B38-	144-8	38-	08-09-144-838-31	30	US-09 144-838-35	US-09-809-391-486	п5-09-888-938-5	00.10.011 400.15
Sequence 8, Appli	Sequence 21, Appl	Sequence 8, Appli	Sequence 16, Appl	Sequence 44, Appl	Sequence 11, Appl	`	Sequence 43, Appl	12 12 1	Sequence 40, Appl		¥2,		Sequence 40180, A	Sequence 29, Appl	`	Sequence 39, Appl	Sequence 38, Appl	36,	~	31,	`	-	Sequence 486, App	Sequence 5. Appli	sequence it, Appl

# ALI-INMENTS

Grant

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PRIOR EPILING DATE: 2000-05-26
PRIOR PRICING UNIMEER: 60,207.727
PRIOR FILING DATE: 2000-05-26
PRIOR ETLING DATE: 2000-10-23
PRIOR ETLING DATE: 2000-11-23
PRIOR PRICING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
SOFTMARE: FASTSEQ FOR WINDOWS Version 4.0
SEQ ID NO 12610
LENGTH: 5795
                                                                                                PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
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Best Local Similarity 83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11289, Application 05/09815242
Patent No. US20020061569Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Xu, H. HOWARD
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Probaryotes
FILE REFERENCE: ELITRA.011A
CURPENT APPLICATION NUMBER: 05/09/815/242
CURRENT FILING LATE: 2001-03-21
PRIOR APPLICATION NUMBER: 50/141 074
PRIOR APPLICATION NUMBER: 50/141 074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Staphylococcus aureus 09-815-242-12610
                  PRIOR FILING DATE: 20 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Haselbeck, Robert
SOFTWARE: FastSEQ for Windows Version 4.0
                                                         PRIOR APPLICATION NUMBER: 60/269,308
                                                                                  PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1127 IKUYET 1134
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Yamamoto, Robert T.
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Zyskind, Judith W.
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                                         2001-02-16
                                                                                2000-12-22
                      14110
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; TYPE: PRT; ORGANISM: Helicobacter pylori
US-09-815-242-11289
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PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

FETCH FILING DATE: 2000-11-23

FETCH APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-23

PRIOR FILING DATE: 2000-12-23

PRIOR FILING DATE: 2000-102-16
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                                                                                                                           US-09-782-874-3
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                                                         Sequence 3, Application US/09782874 Patent No. US20010023067A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification of Essential TITLE OF INVENTION: Prokaryotes FILE PEFEPENCE: ELITRA 011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                               IYPE: PRT
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APPLICANT: Wassenegger, Michael
Riedel, Leonhard
Schiebel, Winfried
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TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING

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JS-09-782-874-3
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JS-09-912-020-350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarit;
              APPLICANT: XU, H. HOWARD

TITLE OF INVENTION. ASSNES TOFNITTE AS REQUIRED FOR FROTTERFATION IN

TITLE OF INVENTION. ESCHERICHA COLI

FILE REFERENCE: ELIFA ODILVI

CURPENT AFFILTATION NUMBER 15, 11, 11, 12, 5

EVICE APPLICATION NUMBER 104,442,704

PRIOR FILING DATE: 2001-07-27

PRIOR FILING DATE: 2001-07-27

PRIOR FILING DATE: 1999-01-27

PRIOR APPLICATION NUMBER: 50,711,405

PRIOR FILING DATE: 1999-01-27

UNDBER OF SEO ID NOS: 485
                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                  APPLICANT: Zyskind, Judith
APPLICANT: Ohisen, Kari L
APPLICANT: Trawick, John
APPLICANT: Forsyth, R. Allyn
APPLICANT: Froelich, Jamle M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                      APPLICANT:
SOFTWARE: FastSED for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/COCKET NUMBER: MEG-1
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 212-596-9000
TELEPAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHAPACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 VEEYFIN 150
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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AFT: "ALL-N BUMSET OS FILING DATE: OB-F-b-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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STRANDEDNESS: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBERS US 08/811 583 FILING DATE: 05-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH 218 amino acids
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                                                                                                                                                                                                                                                                                                   Carr, Grant J.
                                                                                                                                                                                                                                                                             Yamamoto, Robert T.
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RESULT 8
US-04-910-430-27
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; ORGANISM: E. Coli
US-09-912-020-350
                  SOFTWARE: FASISEQ for Windows Versi at 4.0 SEQ ID NO 27 LENGTH: 377
                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27, Application 05/09910430 Patent No. 0520020127235Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 16
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Best Local Similarity
                                                                         CURRENT AFFLICATION NUMBER (15,704,79)0,430
CURRENT FILING DATE: 2001-07-19
EPROP APPLICATION NUMBER: CCT/FFCO/ 7061
EFFOR APPLICATION NUMBER: GB 991342-16
EPROP APPLICATION NUMBER: GB 991342-16
EPROP FILING DATE: 1949-06-09
ENUMBER OF SEQ ID NOS: 34
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Best Local Similarity
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PPIOP APPLICATION NUMBER: 09/594,185

PRIOP FILLING DATE: 2000-06-14

PRIOR APPLICATION NUMBER: EP 96115540.5

PPIOP FILLING DATE: 1096-09-27

NUMBER OF SEQ ID NOS: 23

SOFTWARF: Patentin Ver 2.1
                                                                                                                                                                                                                           APPLICANT: Bollen, Alex
APPLICANT: Leboulle, Gerard
TITLE OF INVENTION: IDENTIFICATION AND MCLECULAR CHARACERIZATION OF
TITLE OF INVENTION: PROTEINS, EXPRESSED IN THE IXODES RICINUS SALIV
FILE REFERENCE: VANUAC29,001CPT
FILE REFERENCE: VANUAC29,001CPT
                                                                                                                                                                                                                                                                                                                         APPLICANT: Godfroi, Edmond
APPLICANT: Bollen, Alex
APPLICANT: Leboulle, Gerarc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: Biotin Genes CURRENT APPLICATION NUMBER: HS/10/03:0.078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Furuichi, Yasuhiro
APPLICANT: Hoshino, Tatsuo
APPLICANT: Kimura, Hitoshi
APPLICANT: Kiyasu, Tatsuya
APPLICANT: Nagahashi, Yoshie
TITLE OF INVENTION: HIGTIN BIOSYNTHIIN GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Kurthia sp
TYPE: PRT
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                                                                                                                                                                                                                                                                                  PROTEINS, EXPRESSED IN THE IXODES RICINUS SALIVARY
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57.18;
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CUPPENT APPLICATION UNMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR PAPPLICATION UNMBER: UP 99/377484
PRIOR FILING DATE: 19-9-12-16
PRIOR PAPPLICATION UNMBER: UP 00/159162
PRIOR APPLICATION UNMBER: UP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
NUMBER OF SEQ ID NOS: 7059
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3-09-738-626-5605
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Publication No. US20030045472A1
GENEPAL INFORMATION:
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Best Local Similarity
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                                                                             SOFTWARE: PatentIn ver.
SEQ ID NO 5606
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APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI KEIKO
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TYPE: PRT
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                                        LENGTH: 511
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SENOH, AKIHIRO
IKEDA, MASATO
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Fred. No. 4.1e+62,
1/ Mismatches (
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: Sequence 10760. Application US/0981524;
: Patent No. 0S20020061569A1
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US-09-770-940-2
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Best Local Similarity
Fig. 5: Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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CORRENT FILING DATE: 2001-03-21
PPTOP APPLICATION NUMBER: 60/191/078
PRIOR FILING DATE: 2000-03-21
PPTOP APPLICATION NUMBER: 60/206.848
PRIOR FILING DATE: 2000-05-23
FEICE AFFLICATION NUMBER: 60/207.727
                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.0%;
Matches 5; Conservative 0
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TITLE OF INVENTION: PROCESS FOR STAFFFIZING PROTEINS IN AN TITLE OF INVENTION: ACIDIC ENVIRONMENT WITH A HIGH-ESTER PECTIN FILE REFERENCE; DYOU14.001APC
                                                            APPLICANT: Kreiberg, J. APPLICANT: Buchholt, H.
                                                                                                        APPLICANT: Christensen, T. APPLICANT: Thorsoe, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR EMPLICATION NUMBER: 60/257 931
FRIOR FILING DATE: 2000-12-22
FRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-05-26
FMICH APPLICATION NUMBER: 60,7242,578
PRIOR FILING DATE: 2000-10-23
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APPLICANT:
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NUMBER OF SEQ ID NOS: 14110
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83.3%;
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Pred. No 4.8e+02:
1: Mismatches (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 570;
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RESULT 14
IS-09-782-874-2
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JS-09-815-242-5093
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LENGTH: 584
Sequence 2. Application US/09782874
                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                  Query Match
77 8%;
Best Local Similarity 57.1%;
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 69/191,078
PRIOR FILING DATE: 2000-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER - 60/269,308
PRIOR FILING DATE: 2001-02-16
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60,257,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER 60/207.727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-23
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Pokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith V
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NUMBER OF SEQ ID NOS: 14110
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Zyskind, Judith W.
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Xu, H. Howard
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SEQ ID NO 14
LENGTH: 32
                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/09144838A Patent No. US20020051996A1
                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. US20010023067Al GENERAL INFORMATION:
                                        EARLIER APPLICATION NUMBER: US 6
EARLIER FILING DATE: 1997-09-04
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.1
                                                                                                                               CURRENT APPLICATION NUMBER, US/
CURRENT FILING DATE: 1998-08-31
                                                                                                                                                                     APPLICANT: Siani, Michael A.
APPLICANT: Wilken, Jill
APPLICANT: Simon, Reyna
APPLICANT: Kent, Stephen B.H.
TITLE OF INVENTION: Modular Protein Cibraries and Methods of Preparation
FILE REFERENCE: GREN. 1207/1010S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 212-596-9090 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION
TELEPHONE: 212-596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US OR/HILS83 FILING DATE: 05-MAR-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NUCLEIC ACL, MOLECULES ENCODING POLYPEPTILES HAVING THE ENZYMATIC ACTIVITY OF AN RNA-DIRECTED ENA POLYMERASE (RDRP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wassenegger, Michael
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AFFILICATION NUMBER US, 00 000, 004
FILING DATE: 08-Feb-2001
CLASSIFICATION: <0nknown:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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15-JUL-1999 (Rel 38, Last annotation update)
Small inducible cytokine A8 precursor (CCLR) (Monocyte chemotactic protein 2) (MCF-2) (Monocyte chemoattractant protein 2).
SCYA8 OR MCP2.
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                                                                                                                                                                                         SEQUENCE FROM N A MEDILINE-95091716; PubMed-7999015;
                                                                                                                                                                                                                                                                                                Mammalia: Eutheria: NCBI_TaxID=9823;
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Blochem Biophys. Res
                                                                                                              Hosang K.K., Knoke I.I., Klaudiny Scheit K.K.:
                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa (Pig).
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                               "Porcine luteal cells express monocyte chemoattractant protein-2 (MCP-2), analysis by cDNA cleming and morthern analysis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro: IPR000827: CC_chemkine_sml.
InterPro: IPR001811; Chemokine_IL8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48 LESYT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LESYT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INDUCTION: BY INTEREERON GAMMA, MITOGERS AND INTERLEUKIN-1. SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE C-C) (CHEMOKINE CC).
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X10802: CAA71760.1; ·.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (kel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9534447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMALL_CYTOKINES_CC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cetartiodartyla; Suina:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata, Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 25; DB
100.0%; Pred. No. 11;
       Commun. 205:148-153(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ×
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9567976BB9422F2A CRC64,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMALL INDUCIBLE CYTOKINE A8
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                                                                                                                                                  J.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 AA.
                                                                                                                                              Wempe F.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 99;
                                                                                                                                                                                                                                                                                                                                           Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                  Wuttke W.W.,
                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                         MEDLINE #99120557; PubMed #9923682; Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doiq Smith D K., Noonan B., Guild B C., deJonge B L., Carmel G., Tummino P.J., Caruso A., Uria-Nickolsen M., Mills D.M., Ives G. Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The waster by non-profit institutions on long modified and this statement is non-ode entities requires a liberuse agreement (over or send an email to licenseeisb-sil.ch).
            -!- CATALYTIC ACTIVITY: Acyl-CoA + 1-acyl-sn-glycerol 3-phosphate CoA + 1,2-diacyl-sn-glycerol 3-phosphates CoA + 1,2-diacyl-sn-glycerol 3-phosphates: second step. -!- PATHWAY: De nove phospholipid (c)-cyyuthesis: second step. -!- SUBCELLUIAR LOCATION: Inner membrane -associated (Potential). -!- SIMILAPITY: BELONSS 10 THE 1-A-YL-SN-GLYCEROL-3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _HELPJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interess, 189700827; CS_shemkine_sml.
Interfr., 189701811, Chemokine_IL8
Pfam; PF00048; ILB; 1.
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                                                                                                                                gastric pathogen Helicobacter pylc:i.";
Nature 307:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori 199 (Campyloba ter pylori 199)
Bacteria: Proteobacteria: epsilon subdivision: Hel
                                                                                                                                                                                                                                                                                                                                                                                                                     1-acyl-sn-glycerol-3-phosphate acyl-transferase (E^ 2.3.1.51) (1-AGP
acyltransferase) (1-AGPAT) (Lysoph-sphatidic acid acyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MODIFIES
                                                                                                -1- FUNCTION: CONVEKTS LYSOPHOSPHALITIC ACID (LPA) INTO PHOSPHATIDIC ACID BY INCOPPOPATING ACYL MOJETY AT THE 2 POSITION.
                                                                                                                                                                                 Trust T.J.
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                        Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9ZJN8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLSC_HELPJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00199; SCY: 1.
PEOSITE: FS0C472; SMALL
                                                                                                                                                                                                                                                                                                                                                                                       PLSC OR JHP1267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES.
                                                                                                                                                               "Genomic sequence comparison of t_{w_{\ell}} unrelated isolates of the human
                                                                                                                                                                                                                                                                                                                                                                                                         (LPAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequency update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAN BIND HEFARIN.
SHEEP: 'N FOUTLIBRIUM (BY SIMILARITY)
 ACYLTRANSFERASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILAPITY: BELONGS TO THE INTERCIPINE BETA FAMILY (SMALL CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248480; CAA88371.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SS-PROT entry is copyright. It is produced through a collaborathe Swiss Institute of Biranformatics and the EMBL outstat pean Bloinformatics Institute. There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chemotaxis, Signal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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BY SIMILARITY.
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                                                                                                                                                                                                                                     King B.L., Brown E.D., Doig P.C.,
deJonge B.L., Carmel G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DR 1;
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                                                                                                                                                                                                    Vovis G.F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        025903;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
1-acyl-sn-glycero1-3-phosphate acyltransferase (EC 2.3.1.51) (1-AGP acyltransferase) (1-AGPAT) (Lysophosphatidic acid acyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL: AE001550: AAD06852.1: --
InterPro: IPR004552: AGF_acyltrn.
InterPro: IPR002123: Acyltransferase.
Piam: PF01553: Acyltransferase; 1.
TIGPFAMS: TIGPON530: AGF_acyltrn: 1.
Phospholipid biosynthesis: Transferase; Acyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann P.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Petersen S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., FittGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley T.M., Cotton M.D., Weidman J.M., Fujil C., Bowman C., Watthey L., Wallin E. Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                          This SWISS-PROI entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pylori.";
Nature 388:539-547(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=26695 , ATC: 711392,
MEDLINE=97394467; PubMed=9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori (Campylobacter pylori).
Bacteria: Proteobacteria: epsilon subdivision, Helicobacter group:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGTAH
                                                                                                                                                                                                                                                                                       -!- FATHWAY. De novo phospholipid biosynthesis, second step.
-!- SUBCELLULAR LOCATION: Inner membrane-associated (Potential).
-!- SIMILARITY: BELONGS TO THE 1-ACYL-SN-GLYCEROL-R-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                             Venter J.C
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SEQUENCE 237 AA; 27188 MW; EH
entiries requires a license agreement (See http://www.ish-sib-ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -I- FUNCTION: CONVERTS LYSOPHOSPHATIDIC ACID (LPA) INTO PHOSPHATIDIC ACID BY INCORPORATING ACYL MOLETY AT THE 2 POSITION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete yenome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 LESYT 208
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les 5; Conserv
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                                                                                                                                                                                                                                                     ACYLTRANSFERASE FAMILY
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Pred. No. 30;
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Best Local Similarity
                                                    Matches
                                                                                                                                                                                                                                                                                                                             Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sitton G.G., Blake J.A., FitzGerald L.M. Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I., everbeek P., Kirkness E.F. Weinstrok G.K., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts F.M., Hurst M.A., Faine B.P., Rerodevsky M., Klenk H.-P., Fraser C.M., Smith H.- Whese C.R., Venter J.C.; "Complete genome sequence of the methanogenic atchaeon, Methanoconccus jannaschil.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methanocaldococcaceae; Methanocaldococcus CBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro: IPR002123; Acyltransfera
Pfam; PF01553; Acyltransferase; 1.
TIGRFAMs; TIGR00530; AGP_acyltrn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR004552; AGP_acyltrn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000636; AAD08393.1; TIGR; HP1348; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib-ch)
                                                                                                         SEQUENCE
                                                                                                                                                                                                         01-NOV-1997 (Rel. 35) Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q58121;
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                                                                                                                                       Hypothetical protein; Transmembran:: Complete proteome
                                                                                                                                                                   EMBI; U67518; AAB98714.1; -.
                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE #96337999; PubMed = 8688087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein MJ0711.
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                                                                                                                          TRANSMEM
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                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright
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106 LESYT 110
                                                                  Local
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                         1 LESYT 5
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NCE 240 AA;
                                                                                                                                                       MJ0711;
                                                   Similarity
5; Conserv
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                                                                                                           322 AA;
                                                      Conservative
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AA; 27745 MW; 2280550EB190BBD5 CPC64;
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35, Last sec
                                                                                                            38631 MW:
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                                                                   100.0%;
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Ng W.V. Kennedy S.P., Mahaliras G.G., Berquist B., Pan M., Shukla H.D. Lasky S.R. Baliga N.S., Thorsson V. Sbrogna J. Shukla H.D. Lasky S.R. Baliga N.S., Thorsson V. Sbrogna J. Swartzell S., Welf D., Hall J., Dahl T.A., Welf R., Goo Y.A. Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W. Maddocks D.G. Jabionski P.E., Kiebs M.P., Angewine G.M., Cale H. Isenbarger T.A., Peck R.F., Pohischroder M., Spudich J. L., Tung K.-H. Alam M., Freitas T., Hou S., Danserder M., Spudich J. L., Lechis F. Chamber T. Hou S., Danserder M., Chamber T. H., Lowe T.M., Lang P., Piley M., Hood L., DasSarma S., "Genome sequence of Halobacterium species NRC-1.";

Proc. Natl Acad Sci H.S. A. 97:12176-12181(2000).

1- FUNCTION: CAPALYZES THE 1.3-ALLYLIC KEAKKANUEMENI OF THE HOWALLYLLY SHESTPATF ISSAPENIENEL (IPP) TO JIS ALLYLIC ISOMEP, DIMETHYLALLYL DIPHOSPHATE (DMAPP) (BY SIMILARITY).

1- CAMBLYTIC ACTIVITY: ISSPENIENCY diphosphate - dimethylallyl
                                                                                                                                                 Query Match
                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I2_HALN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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Ng W.V., Clufo S.A., Smith T.M., Bumgarner R.E., Baskin D., Faus
Hall B., Torerz C., Sero T., Slagel T., Hood L., DasSarma S.;
"Snapshot of a large dynamic replicanting halophilic archaeun:
megaplasmid or minichromosome?";
Genome Res. 8-1131-1141(1948)
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: AF016485; AAC82844.1; ALT_INIT.
EMBL: AF016485; AAC82933.1; ALT_INIT.
EMBL: AE005145; AAC820768.1; -
EMBL: AE005169; AA;21040.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9HHE4; 054623;
                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                   Isomerase; Isoprene biosynthesis: Flavoprotein; FMN; NADP; Plasmid; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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NCBI_TaxID=64091:
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Plasmid pNRC100, and Plasmid pNRC200
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(ENII OR VNG5084G OR H0560, AND (ENIZ OR VNG5213G OF H1696) AND (ENIZ OR VNG6445G).
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16-00T-2001 (Rel. 40, Last sequence update)
16-00T-2001 (Rel. 40, Last annotation update)
16-00T-2001 (Rel. 40, Last annotation update)
15opentenyl diphosphate delta-isomerase (EC 5 3.3 2) (TFP isomerase)
                                                                                                                                                                                                                                                                                                                                 Pfam: PF01070; FMN_dh: 1
                                                                                                                                                                                                                                                                                                                                                                 InterPro: IFR003009; FMN_enzyme.
InterPro: IFR008262; FMN_hydxyac_dh
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                                                                      Local Similarity 100 hes 5: Conservative
1 LESYT 5
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SIMILARID: BELOWGE TO THE TEP ISOMERASE TYPE 2 FAMILY
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                                                                                                                                                                                                                           360 AA; 38342 MW; 67B14178071D3164 CRC64;
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Theres 5: Conserve
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                                                                                                                                                                                                                                                                       RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Milecular, genetic, and blochemical characterization of one serving pene of Methalosarchna barkeri Fusaro.";

J. Bacteriol. 178:5797-5802(1996).

-i- CATALYTIC ACTIVITY: O-phospho-L-serine + 2-oxoglutarate = 3-phosphonooxypyruvate + L-glutamate.

-i- COFACTOR: PYRIDOXAL PHOSPHATE

-i- COFACTOR: PYRIDOXAL PHOSPHATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-007-2001 (Pel 40, Last annotation update)
Phosphoserine aminotransferase (EC 4.6.1.52) (FSAT).
                                                                                                                             ERF1
                                                                                                                                                                       15-00T-2001 (Rel. 40, Created)
16-00T-2001 (Rel. 40, Last Sequence update)
16-00T-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                           ERF1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro: IPR000192; AminotransfV.
PROSITE: PS00595; AA_TRANSFER_CLASS_5: FALSE_NEG.
Serine biosynthesis; Pyridoxine biosynthesis; Transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE-96422013; FubMed-8824630; Metcalf W.W., Zhang J.K., Shi X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-00T-1996 (Rel. 34, Last sequence of 15-00T-2001 (Pel. 40, Last annotation
                              SEQUENCE FROM N.A. PubMed=10844194;
                                                                           Eukaryota: Diplomonadida: Hexamitidue: Giardiinae: Giardia
NCPI_TaxID~5741;
                                                                                                                                                         Eukaryotic peptide chain release factor subunit 1 (eRF1) (Eukaryotic
                                                                                                                                                                                                                          Q9NCP1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-00T-1945 (Rel 34, Created)
 "Evolution of the eukaryotic translition termination system: origins
                                                                                                            Giardia lamblia (Giardia intestina:(s)
                                                                                                                                            release factor 1).
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                Inagaki Y., Doolittle W.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 LESYT 116
                                                                                                                                                                                                                                                                                                                      211 LESYT 215
                                                                                                                                                                                                                                                                                                                                                   1 LESYT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMINOTRANSFERASES.
                                                                                                                                                                                                                                        _GIALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METBA
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhang J.K., Shi X., Wolfe R.S.; enetic, and blochemical characterization of the serc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / DSM 804;
                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 100.0%; Pred No. 51; itive 0: Mismatches
                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ipdate)
                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1: Length 370;
                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a collaboration
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3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no was modified and this statement is not removed. Usage by and for removable entities requires a limits against and the properties of send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PFoT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of release factors.";
Mol. Biol. Evol. 17.882 889(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-mt-1999 (Pel 38, Last annotation update)
Retinoic acid receptor RXK-gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: Directs the termination of mascent peptide synthesis (translation) in response to the termination codons UAA, UAG and
                                                                                                                                                                                                                                                                                               Blumberg B., Mangelsdort D.J., Dyck J.A., Bitther D.A., Evans R.M., de Robertis E.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Amphibia: Batrachia; Amura: Mesobatrachia, Fipóidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota: Metazoa, Chordata: Oraniata; Vertebrata: Estelessioni:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RXRG OR NR2B3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RXRG_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF03463; eRF1_1; 1.
Pfam; PF03464: eKF1_2; 1.
Pfam; PF03465; eRF1_3; 1.
TIGREAMS; TIGRECIUE: eRF: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro: IPR005140: eRF1_1.
Interpro: IPR005141: eRF1_2.
Interpro. IPR005142: eRF1_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro: IPR004403, eRF1.
InterPro: IPR005140; eRF1_
                                                                                                                                                                                                                     Proc.
                                                                                                                                                                                                                                                            retinoid 'X' receptors and retinoic acid receptors in the Xenopus
                                                                                                                                                                                                                                                                                                                                        MEDLINE-92196110, FubMed-1312717;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                            "Multiple retinoid-responsive receptors in a single cell: families of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 LESYT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LESYT 5
PERMITION: INVOLVED IN RETINCTC ACID RESPONSE PATHWAY. BINUS
9-CIS RETINCTC ACID (9C-RA) (BY SIMILARITY).

SUBNUT: HOMODIMER OF HETERODIMER (BY SIMILARITY).

SUBCELLULAR LOCATION: Nuclear:
SUNCELLULAR LOCATION: Nuclear:

DEVELOPMENTAL STAGE: IT IS SINTHESIZED DURING OOGENESIS AND
DEVELOPMENTAL STAGE: IT IS SINTHESIZED DURING COMSENST AND
PERSISTS IN THE CLEAVING EMBRYO AT APPROXIMATELY CONSTANT LEVELS
UNILL IT IS DESPACED JUST REPROPE GASTPULATION.

LOMANIS: COMPOSED OF THREE COMMAINS: A MODULATING N-TERMINAL DOMAIN.

A DNA-BINDING ECMAIN AND A C-TERMINAL STEROID-BINDING COMMAIN.

SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.

NR2 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: BELONGS TO THE EUKAPYOTIC RELEASE FACTOR 1 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (translation) in response to the termination codons UAA, UAG UGA (By similarity). SUBUNIT: HETERODIMER OF TWO SUBUNITS, ONE OF WHICH BINDS GTF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P46055; 1DT9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF198107; AAF74402.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51029 MW; EE185FFFD1F0C943 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%: Score 25; DB 1; bength 457: 100.0%: Fred. No. 64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         470 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is in no way
of for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ,,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Вþ
   MURD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2N_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities regulares a license agreement (See http://www.isbestbeech.andernore)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright If is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC 1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DUN-2002 (Rel. 41, Last annotation update)
10-N-acetylmuramoylalanine--D-globamate ligase (EC 6.3.2.9) (UDF-N-acetylmuramoyl-Loalanyl-D-glutamate synthetase) (P-glutamic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00047; STROIDFINGER
Procom PD000035; Znf_C4steroid: 1
                                                                                                                                                                                                                MEDLINE-9879270; PubMod=9665876;

Fraser C.M., Norris S.J., Weinstork G.M., White O., Sutton G.,

Praser C.M., Norris S.J., Weinstork G.M., White O., Sutton G.,

Podson B., Gwith M., Hickey E.K., "layton P., Ketchum K.A.,

Sodergren E., Hardhum I.M., McLood M.P., Salzherg S., Peterson J.,

Sodergren E., Hardhum I.M., McLood M.P., Salzherg S., Peterson J.,

Schalak H., Bichardson D., Howell I.K., Childmeharam M., Ofterback I.,

McDonald L., Artiach P., Fowman C., Otton M.D., Fujii C., Garland S.,

McDonald L., Artiach P., Powman C., Otton M.D., Fujii C., Garland S.,

Hatch B., Horst K., Roberts K., Stodusky M., Weldman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00430; HOLI;
SMART: SM00399; ZnF_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00104; hormone_rec; 1 Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro IPR000536, Hormone_rec_lid.
InterPro IPR001723; Stdhrmn_receptor.
InterPro IPR001f2P Onf_04steroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                Spirochete.";

Shipone 291-375-388(1998).

Shipone 291-375-388(1998).

SHIPONE CELL WALL FORMATION CHATALYZES THE ADDITION OF DEGLOTAMATE TO THE NUCLEOTIDE PRECURSOR UDP-N-ACETYLMURAMOYL-LOGIC GLOTAMATE TO THE NUCLEOTIDE PRECURSOR UDP-N-ACETYLMURAMOTE TO THE NUCLEOTIDE TO THE NUCLEOTIDE TO THE NUCLEOTIDE TO THE NUCLEOTIDE TO THE NUCLEOT
                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Nichols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Preponema pallidum.
Bacteria: Spirochaetales, Spirochaetaceae, Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MURD OR TP0903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adding enzyme)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MURD_TREPA
083873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zinc-finger; Multigene family
DCMAIN 1 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor; Transcription regulation: DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART: SM00399; ZnF_C4; 1.
PROSITE; PS00031; NHCLEAR_RECEPTOR: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSFAC; T01360;
                                                                                                                                                                                      Venter J.C.;
                                                                                                                                                         "Complete genome sequence of Trepodema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            408 LESYT 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LESYT 5
ALANINE (UMA) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P19793; 2NLL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111443,
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236
470 AA;
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2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOT_AMMOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51925
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LIGAN: BINDING (BY SIMILARITY).
: DD31720C53C53A5F CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C4-TYFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEAR RECEPTOR-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MODULATING (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      532 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                           Garland S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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$70_CHICK
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Best Local Similarity
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                                                                                                                                                                               HSP70 gene.";
J. Biol. Chem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Heat shock 70 kDa protein (HSP70).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken)
Eukaryota, Metazca, Cho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam PF01225 Mur_ligase, Pfam PF02875 Mur_ligase_C TIGRFAMs TIGP01087 murp:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bilinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
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Pfam; PF00012; HSP70; 1.
PRINTS; PR0c301; HEATSHOCK70
                                                                 PIR: A25646; A25646.
HSSP: P08109: 1CKR
                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                  J. BIOI. Chem. 261:12692-12699(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-86304452: PubMed-3017985; Morimoto R.I., Hunt C., Huang S.-Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HS70_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.fsb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                          InterPro: IPR001023; Hsp70.
                                                                                                                                                                or send an email to licensedisb-sib.ch)
                                                                                                                                                                                                                                                          the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                "Organization, nucleotide sequence, and transcription of the chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-9031,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-binding; Complete proteome
NP_BIND 124 130 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000713;
InterPro; IPR004101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FATHWAY: Feptidoglycan biosynthesis.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By Similarity).
-!- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE 532 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptidoglycan synthesis; Cell wall; Cell division; Ligase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        385 LESYT 389
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TP0903; -.
                                                                                                                   J02579; AAA48825.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AE001259; AAC65856.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata: Craniata: Vertebrata: Enteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 25; DB 100.0%; Pred. No. 76;
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RESULT
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                                                                                                                         entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-s.h.ch).
                                                                                                                                                                   This SWISS-PEOT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95130116; PubMed=7829106;
Bonnydastle L.L.C., Yu C.-E., Hunt F.E., Trask B.J., Clancy K.P.
Weber J.L., Patterson D., Schellerterg G.D.;
"Cloning, sequencing, and mapping of the human chromosome 14 heat
shock protein_gene (HSPA2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryuta, Metakwa, Chordata; Cranista, Vertebrata: Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE: PS01036; HSP70_3; 1. ATF-binding: Heat shock; Multigene family SEQUENCE 634 AA: 69750 MW: 4270F7F08D
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PROSITE; PS00329; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                              Poux A.-F., Nguyen V.T.T. Squire I.A. Cox D.W.;
"A heat shock gene at 14q22: mappil, and expression.";
"Hum. Mol. Genet. 3:1819-1822(1994)."
-!- FUNCTION: IN COOPERATION WITH-"HEP CHAPEPONES, HSP70S STABILIZE
                                                                                        EMBL; L26336; AAA52698.1; -. EMBL; U56725; AAD11466.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-126 FROM N.A. MEDLINE-95152505, PubMed-7849706,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goralski T.J., Krensky A.M.;
Submitted (APR-1996) to the EMBL/WeaRank/EDBT databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
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EMBL, U10149, HSSP; P19120;

3HSC

AAD11466.1; -. AAC50076.1; -.

MIM; 140560;

InterPro; Genew;

FF00012: HSP70: 1 HGNC:5235; HSPA2. IPR001023: Hsp70

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the FMRL outstation the European Bioinformatics Institute. There are no restrictions on I use by non-profit institutions as long as its content is in no wondified and this statement is not removed. Usage by and for commerci entities requires a library agreement (See http://www.isb-sib-ab/aurounce
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Primosomal protein N' (Replication factor Y).
PRIA OR CPN0924 OR CP0992.
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ProDom: PD000089; Hsp70: 1.
PROSITE: PS00247: HSP70_1: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kalman S . Mitchell W . Marathe R. Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis P.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydia pneumoniae (Chlamydophila pneumoniae)
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
NCBL_TaxID=8355#;
                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                              MEDLINE=20330349; PupMed=10871362;
                                                                                                                                                                                                                                                                                                 STRAIN-J138
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                       "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia preumoniae AR39.", % \left( \frac{1}{2}\right) =\frac{1}{2}\left( \frac{1}{2}\right) ^{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20150255; PubMed=10684935;
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                                                                                                             SIMILARITY: BELONGS TO THE HELICASE FAMILY, PRIA SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 - 385 - 389 (1999)
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100.0%; Pred. No. 94;
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                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWiss Institute of Bicinformatics and the EMBL outstation—the European Rioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial extitles requires a license agreement (For Mit) [www.isbesil.ch.] of send an email to licenselisbesil.ch.]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=MoPn / Nigg;
MEDLINE=20150255; PubMed=10684935;
Peed T.D. Brunham P.C. Shew C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequency update)
16-OCT-2001 (Rel. 40, Last annotation update)
Primosomal protein N' (Replication factor Y).
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SMAPT: SM00487; nFXDc; 1.
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Bacteria; Chlamydiales; Chlamydiacone; Chlamydia
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DNA replication: DNA-binding: ATP-winding: Helicase: Primosome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequences of Chlamydia trachomatis MoPa and Chlamydia pneumoniae AR39.";
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InterPro: 1PR001410: DEAD.
InterPro: 1PR001650; Helic
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FUNCTION: PEDURNIZES A SPECIF: HAIPPIN SEQUENCE ON PHIX SEDNA.

THIS STRUCTURE IS THEN RECORD. TED AND BOTHEN BY PROTEINS PRIB AND

PRIC. FORMATION OF THE PRIMOSOME PROCEEDS WITH THE SUBSEQUENT

ACTIONS OF LINAB, DUAC, DNAY AND PRIMASE, PRIA THEN FUNCTIONS AS A

HELICASE WITHIN THE PRIMOSOME (BY SIMILARITY).

SIMILARITY: BELLINGS TO THE HELDASE FAMILY PRIA SUBFAMILY.
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                                                         TC0159;
                                                                                    AF002283; AAF39035.1;
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Similarity 100.0%;
5; Conservative 0
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749 AA;
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C4-TYPE (POTENTIAL).
; 23103802F3897B4B CFC64;
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Pred No 1 1e+02:
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Helicase\_C

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IA_CHLTR
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                 ZN_FING
                                                                                          Pfam: PF00271; helicase_C: 1.
SMART: SMO0487: DEXPC: 1.
SMART: SM00490: HELICC: 1.
TIGREAMS: TIGRU0595; priA: 1.
DNA replication: DNA-binding: ATP-binding; Helicase: Primosome:
                                                                                                                                                                                                                                                        Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Primosomal protein N' (Replication factor Y).
PRIA OR CT778.
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DNA replication: DNA-binding; ATP-binding; Helicase; Primosome;
                                Zinc-finger: Complete proteome
241 248 AN
SITE 337 340 DE
ZN_FING 458 470 C4
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MEDLINE=99000809: PubMed=9784136;
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Bacteria: Chlamydiales: Chlamydiaceae: Chlamydia.
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O84783;
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SMART; SM00487; DEXUC; 1.
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   SEQUENCE
                                                                                                                                                                           InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helicase_C.
InterPro; IPR005259; PriA.
                                                                                                                                                                                                                               EMBL; AE001350: AAC68373.1; -.
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470 C2
501 C2
: 84764 MW;
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   84831 MW:
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C4-TYPE (POTENTIAL).
CD4CFEE77FC4AB05 CRC64:
C4-TYPE (POTENTIAL).
C4-TYPE (POTENTIAL).
C9186184385C5E45 CRC64;
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Query Match 100.0%; Score .5; DB 1; Length 753;
Best Local Similarity 100.0%; Fred. HJ. 1.1e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 1 LESYT 5
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Db 379 LESYT 383
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Search completed. April 8, 2003, 12:02:14 Job time : 15:0833 secs

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Listing first 45 summaries
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ເximum DB seq length: 200000ໂປປິວ
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Gapop 10.0 , Gapext 0.5
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36
1 IKEYFTS 7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	SCOLE	Match	Match Length DB	80	ID	Description
· ;	1 1 1 2 1 2 1	0.001	7	당 :	AAY49696	ecrpat OffdE I-AiH
	32	88.9	204	23	ABP38988	Staphylococcus epi
~	يد) 13	(B)	#> (-) (-)	Ē	NAM23792	cytidine monophosp
_	٦2	98.9	422	18	AAW10735	Porcine CMP-N-acet
٠,	32	cro cro	- J 1.1 (0)	ار ع نب	ABF26246	Streptococcus poly
-	31	86.1	1460	22	AAG70745	s cerevisiae apopt
~	.) د	83.3	150	2	AAU29339	Novel mar regulate
4	317	81.1	150	2.2	AAGGRITE	Escherichia coli p
_	30	83.3	13 00 00	t	AAG42212	Arabidopsis thalia
_	30	83.3 3.3	402	23	ABB53504	Lactococcus lactis

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	Š	AAY25TPS	AARIOAGO	AAFOORGR	لغر	1.80	AACOB1+5	-	. 20	ū	1	. ,	1.	4950	* .	AAU37(-17	9,	<u>ت</u>	, [B	180	645	694	094	AAG564 = 9	95	$\vdash$	Ś	1831	AAB183 44	547	G153	58	B633	-	ABB92947
	19 buman parvov	Frythrovirus V9 VP	arvo virus B19	NA-direc	s B14	is that	is thal	idopsis that	idopsis tha	cobacter pyl	Ş	H. pylori CHPO 126	seci	eria monoc	Peptide derived in	hylococcus a	9116	sophila	taphylococcu		rabidopsis t	ophila me	ila me	sis t	lanes sp a	Actinoplanes sp. a	Cyclase encoded by	smodium falci	asmodium falc	ccus lact	Novel human diagno	ila n	la me	dally	11y =

### ALICNMENTS

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RESULT 1
AAT49696
ID AAT4
Non-religional degenerative disease FIV-1 envelope protein ap120; taxio nearth accessory offs1 cells chemokine viral infection; courts1 will depth, on webbl path, becompathy memory loss; dementa; depression, psychosis; opportunistic infection;
                                                                                                                                                                                                                                                                                        HIV:1 gp120 indused neuronal sell death inhibiting poptide #2.
                                                                                                                                                                                                     neurotoxicity; inflammatory neurological disease; multiple sclerosis; tropical spastic paraparesis; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                          AAY49696;
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        WPI; 1999-633695/54.
                                 Pert C, Ruff M;
                                                        (ADIM:) ADVANCED IMMUNIT INC
                                                                                  O6-APP-1998
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                                                                                                                                                                                Synthetic.
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                                                                                         ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960, the sc epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Such conditions especially associated with HIV infection include encephalopathies, neuropathies, memory loss, dementia, depression, psychosis and opportunistic infections. The peptides act as antagonists
cycle or inhibit S. epidermidis infection. N.B. The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-1958,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of gpl20-mediated neurotoxicity and subsequent neuronal degeneration. This enables therapeutic treatment of HIV infection and other inflammatory neurological diseases, including multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptides are useful for treating symptoms caused by neuronal cell loss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY49695 and AAY49696 represent peptides which inhibit HIV-1 gp120 induced neuronal cell death. Pharmaceutical compositions containing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 11; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New peptides useful for inhibiting human immuno-deficiency virus type (HIV-1) gpl20 induced neuronal cell death \,
                                                                                                                                                                                                                                                                                                                                                                           Disclosure: SEQ ID 3833: 267pp: English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Doucette-Stamm LA, Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-AUG-1997;
08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6380370-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP38988 standard; Protein; 204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tropical spastic paraparesis and Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid encoding a Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IKEYFTS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
es 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002-381255/41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epidermidis, open reading frame, OPF, hasterial infection, gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-064964P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-055779P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9838 8134801.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Best Local Similarity
Thinks 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         끍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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SQ
                                                                                   hybridisation assays, and are used to inhibit expression of the protein, i.e. as antisense molecules for traitment of tumours, particularly those of high metastatic potential. Cells that have been modified so that they no longer produce the protein are used to produce NeuSGC-free glycoconjugates for therapeutic use. The DNA encoding the protein is used to produce recombinant protein and detection of the gene, normally durmant, can be used to diagnose tempores. Glycoproteins that lack NeuSGC mure closely resemble human products and are suitable for long term therapy since they contain no non-random epitopes (NeuSGC-containing
                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a new isolated protein cytidine monophospho-N-acetylneuramic acid hydroxylase, which is uncontaminated by cytochrome b5 or cytochrome b5 rejuctase. The protein is produced by exogenous DNA in prokaryotic or eukaryotic cells and it catalyses conversion of CMP NewSor (NewSor and NewSor N-acetyl or glycosyl-neuraminic acid respectively). Oligonucleotides which hybridise to CMA Accessing the protein are used to take the protein acids by protein are used to take the protein acids by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New CMP N-acetyl-neuraminic acid hydroxylase and related DNA - used esp. to delete enzyme activity in mammalian cells, allowing product of glycosprotein(s) without N-glycosyl-neuraminic acid suitable for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-SEP-1995;
07-,UUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-1996:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytidine monophospho-N-acetylneuram': acid hydroxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW23792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW23792 standard; Protein; 422 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USPIO web site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 32-33; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :IAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haselbeck A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POEF ) BORHFINGER MANNHFIM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CMP-Neu5Ac hydroxylase; CMP-Neu5Gc h, disxylase, enzyme activity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 VKFYFTA 201
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                                                                  are immunogenic in humans;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytochrome
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71.4%;
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Pred. No 97;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumour
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Query Match

Score 12:

DB 18; Length 422;

Sequence

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BP26246
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X ABP2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                            AAW10735 represents a parcine cytidine mano phosphate (CMF) N-acetyl-neuraminic acid (CMP-Neu5Ac) hydroxylase enzyme. The enzyme catalyses the conversion of CMP-Neu5Ac to CMP-Neu5Cc (cytidine monophosphate-N-qlycoloylamiraminic acid). Antisense sequences of this STNA sequence are used for the production of CMP-Neu5Ac hydroxylase-deficient mammalian cells. The modified cells are useful for the production of recombinant glycoproteins lacking N-glycoloylaminic acid side
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-acetyl-neuraminic acid; Neu5ac; sialic acid; porcine; CMP; cytidine monophosphate; antisense therapy; recombinant production; N-glycoloylneuraminic acid side chain deficient; erythropoietin.
                                                                                                                                                                                                                                                                                                                                                                                                                    Porrine CMP-N-acetyl-neuraminic acid hydroxylase - catalyses conversion of CMP-Neu5Ac to CMP-Neu5Gc, anti:sense sequences of DNA encoding CMP-N-acetyl-neuraminic acid hydroxylase are used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW10735 standard: Protein: 422 AA
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              ABP26246;
                                          ABP26246 standard; Protein; 728 AA
                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                    chains, e.g erythropoietim.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa
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Nes 6: Conserv
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                                                                                                                                                                               Score 32: DB 18;
Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.9e+02;
                                                                                                                                                                    Mismatches
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                                                                                                                                                                                              Length 422:
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RESULT 6
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine meningitis; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           streptococcus/GBS (Streptococcus addiactiae) of group A streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (1), nucleic acids encoding (1), ABN66044-ABN7526 and antibodies that bind (1) are used in the manufacture of medicaments for the treatment of prevention of infection of disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-00%-2000: 2000GR-0026333.
24-NOV-2000: 2000GB-0028727.
07-MAR-2001: 2001GH-0005640.
S cerevisiae apoptosis associated protein YIL112W
                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus that is prevented or invated may be meningitis. Neelele acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography. Immunoassays, and listinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding (1) are used to detect Streptococcus in a biological sample. (1) is used to abtermine whether a compound binds to biological sample. (1) is used to abtermine whether a compound binds to (1). A composition complishing (1) or a nucleic acid encoding (1), may be used as a vaccine or diagnostic composition. The disease caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 3318; 4525pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-352536/38.
N-PSDB; ABN66877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wn20n234771-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus polypeptide SEQ ID NC 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUL-2002 (first entry)
                                        27-JUL-2001
                                                                                                                  AAG70745 standard; Protein; 1460 AA
                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a protein (ABP25413-ABP30895) from group B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tettelin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u> 24-001-2601: 2661W6-GP04789</u>.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for detecting a compound that binds to the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Telford J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENO-) INST GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHIR-) CHIRON SPA.
                                                                                                                                                                                                               131 VKDYFTS 137
                                                                                                                                                                                                                                                   1 IKEYFTS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Masignani V,
                                                                                                                                                                                                                                                                                                                                                                      728 AA;
                                                                                                                                                                                                                                                                                           Conservative
                                      (first entry)
                                                                                                                                                                                                                                                                                                             88,98;
71,48;
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                                                                                                                                                                                                                                                                                                             Score 32, DB 23;
Pred No. 3.3e+02;
                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                              DB 23;
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                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                Length 728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fraser C;
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1atches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides the protein and coding sequences of a number of apoptosis associated proteins from the yeast Saccharomyces cerevisiae and the fungus Candida albicans. These can be used to identify treatments for fungal and yeast infections, for proliferative diseases and for apoptosis related diseases such as autoimmune diseases, ischaemia and neurodegeneration. The present sequence is one of the S. cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and neurodegeneration. The proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yeast and tungal nucled acids encoding proteins involved in a pathway leading to programmed cell death, useful for treating proliferative disorders, yeast and fungui infections, or for preventing apoptosis in certain diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU29339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU29339 standard: Protein: 150 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1190 LKEYYTS 1196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-357042/35.
N-PSDB; AAH29781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nelissen BJM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contreras RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (JANC ) JANSSEN PHARM NV
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Levy SB,
                                                                                              10-MAR-2000: 2000US-188362P
                                                                                                                                            08-MAR-2001: 2001Wo-US07478
                                                                                                                                                                                                                                           WO200170776-A2
                                                                                                                                                                                                                                                                                         Escherichia coli.
                                                                                                                                                                                                                                                                                                                                    mar regulated polypeptide; NIMR; microbial infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                     Novel mar regulated protein (NIMR) #11.
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                                              (TUFT ) TUFTS COLLEGE
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5; Conserv
Barbosa TM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99EP-0870141
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Reekmans RJ;
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71.4%;
  Alekshun MN
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Pred. No.
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RESULT 8
AAG98376
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     Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a newly identified mar regulated (NIMR) polypeptide activity. The method comprises contacting an NIMR polypeptide with a test compound under interaction conditions, determining the ability of the compound to modulate the activity or expression of the polypeptide, and selecting the modulators. NIMR nucleic acids and polypeptides are used in the treatment of microbial infections, and in screening for modulators of NIMR expression and activity. These modulators can be used to reduce the infectivity of a microbe on a surface, and the virulence of a microbe in a subject suffering from an infection. AAN29329-AAN29379 represent Escherichia coli NIMR amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             identifying compounds that modulate a newly identified mar regulated polypeptide activity, useful as antimicrobial compounds, involves contacting the polypeptide with a test compound \cdot
The present invention describes a purified or isolated nucleic acid sequence (I) consisting essentially of one of the 93 nucleotide sequences given in AA881202 to AA481294, where expression of the nucleic acid in a microorganism is capable of lightly proliferation of a microorganism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG98376;
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                                                                                                                    Novel nucleic acids encoding proteins required for Escherichia coli proliferation, useful for screening for antimicrobial agents - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli; identification; proliferation; microorganism; antimicrobial, antibacterial; antibactic; gene therapy; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli protein sequence ED, ID NO:424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG98376 standard; Protein; 150 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method of identifying compounds that moinlate
                                                                                     Claim 19; Page 544; 596pp; English
                                                                                                                                                                      N-PSDB; AAH81432.
                                                                                                                                                                                                                          Forsyth RA,
                                                                                                                                                                                                                                                                                                                            19-DEC-2000; 2000WO-US34419.
                                                                                                                                                                                                                                                                                                                                                              05-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                               W0200148209-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             bacterial growth inhibition.
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                                                                                                                                                                                                                                                          (ELIT-) ELITRA PHARM INC
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                                                                                                                                                                                                                        Ohlsen KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Pred. No. 1.8e+02;
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(I) have antibacterial and antiblotic activities, and can be used in gene therapy. Expression of (I) in a microorganism inhibits proliferation of the microorganism, and the manufactured antiblotic is useful for reducing the activity or level of a gene product required for proliferation of a microorganism in a subject, specifically humans. The nucleic acids that inhibit bacterial protein or proliferation can be used as antisense therapetics for killing bacteria. It additions to therapeutic applications, the nucleic acid sequences complementary to sequences required for proliferation can be used as diagnostic tools. Sequences that are specific for particular species of microorganisms can be used as probes to identify particular species of microorganisms can be used as probes to identify particular information species in collinal species to hadellies to AAG94431, and AAAB1484 to AAAB14844 to AAAB
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25-FEB 1999
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01-APR 1999
01-APR 1999
16-APR 1999
16-APR 1999
23-APR 1999
                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO. 52616.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          termination sequence
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99US-0125788
99US-0125264
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99US-0127452
99US-0128714
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20-MAY-1999
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30-JUN-1999;
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Tür- 80
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28 - JUN -
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19-JHL-1999
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9 907 - 0144 35
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qqrs-0139456.
99US-0139457.
99US-0139458.
99US-0139458.
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99US-0138094.
99US-0138540.
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99US-0135629
99US-0136021.
99US-013632.
               9905-0145087.
9905-0145089.
9905-0145192.
9905-0145145
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9905-0139119.
9905-0139452
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99US-0141287.
99US-0141842.
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9905-0145088
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9905-0137502
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99US-0135124
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99US-0134219.
                                                                     99US-0145085
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990S-0144814
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9905-0144005
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9908-0142977
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99US-0142055
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99US-0140354
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99115-0139460
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8-0134370.
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27-JUL-1999 28-JUL-1999 02-AUG-1999 02-AUG-1999 03-AUG-1999 04-AUG-1999 05-AUG-1999 05-AUG-1999 06-AUG-1999 09-AUG-1999 09-AUG-1999 09-AUG-1999

9908-0147038. 9908-0147204. 9908-0147302. 9908-0147192.

990S-0145951. 990S-0146386. 990S-0146388.

9908-0146389

9908-0145276. 9908-0145276. 9908-0145918.

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RESULT 10
ABB53504
                                                    Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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25-007-1944
25-007-1944
25-007-1944
26-007-1949
26-007-1944
28-007-1944
28-007-1944
28-007-1944
                                                                       The present invention is related to a Lactococcus lactis nucleotide sequence (ABB90521) and related proteins (ABB300521). The nucleic acid sequence is useful in the Abbattin and/or amplification nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent world017334 (gublished 18-007-290) which is available in electronic format directly from WIPO at ftp.Wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lactococous lactis IL1403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lantoconcus lactis protein rgpA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB53504 standard; Protein; 402
                                                    Sequence
                                                                                                                                                                                                                                        Claim 6; SEQ ID No 206; 2504pp; French.
                                                                                                                                                                                                                                                                             New nucleotide sequence useful in the identification or Lactococcus
                                                                                                                                                                                                                                                                                                                                Bolotine A, Sorokine A, Renault F. Ehrlich SD;
                                                                                                                                                                                                                                                                                                                                                                                     11-APR-2000: 2000FR-0004630.
                                                                                                                                                                                                                                                                                                                                                                                                               11-APP-2000;
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                                                                                                                                                                                                                                                               lactis and related species -
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5; Conserv
                                                     402 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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9908-0161004

9908-0161406

9908-0161359

9908-0161350

9908-0161361

9908-0161920

9908-0161920

9908-0161931

9908-0161931
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Pred. No. 3e+0
2; Mismatches
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                           DB 23; Length 402;
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23-AUG-1999; 25-AUG-1999; 26-AUG-1999; 27-AUG-1999;

9908-0150884. 9908-0150884. 9908-0151065.

20-AUG-1999; 23-AUG-1999;

990S-0149723. 990S-0149929. 990S-0149902. 990S-0149930.

20

20 - AUG 18-AUG-1999

27-AUG-1999 27-AUG-1999

99US-0151066 99US-0151080

07-SEP-1999

99US-0151303. 99US-0151438. 99US-0151930. 99US-0152363.

9908-0153070. 9908-0153758. 9908-0154018. 9908-0154039.

16-AUG-1999; 17-AUG-1999;

990S-0149358. 990S-0149175. 990S-0149426. 990S-0149722.

13-AUG-1999

99US-0148341. 99US-0148565.

-1999 -1999

9905-0148684

AUG

99US-0147935. 99US-0148171. 99US-0148319.

99US-0147303. 99US-0147416.

99US-0147250

99US-0147493.

08-00T-1999; 12-00T-1999; 13-00T-1999;

99US-0158369.

9905-0159294. 9905-0159294. 9905-0159295. 9905-0159329. 9905-0159330.

21-0CT-1999; 21-0CT-1999; 21-0CT-1999; 22-0CT-1999; 22-0CT-1999;

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1 IKEYFTS 7

14-0CT-1999; 14-0CT-1999; 18-0CT-1999;

14 -OCT

9908-0159331

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21-00T-1999) 21-00T-1999)

99US:0159638 99US:0159584 99US:0150741 99US:0150767 99US:0150770 99US:0150710 99US:0150814 99US:0150815 99US:0150881

29-SEP-1999; 04-OCT-1999; 05-OCT-1999; 06-OCT-1999;

24-SEP-1999; 28-SEP-1999;

9908-0156458

9908-01

23-SEP-1999; 20-SEP-1999

22-SEP-1999 16-SEP-1999 15-SEP-1999 13-SEP-1999 10-SEP-1999

99US-0154779 99US-0155139

06-00T-1999 07-00T-1999

9905-0158029

9908-0157865

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ESULT 11
BB92997
D ABB92
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aB891466
b AB891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying plant target proteins for herbicidally active compounds, comprising allyning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; SEQ ID NO 2208: 261pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI: 2002-259010/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Herbicidally active polypeptide SEQ ID NO 2208.
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Arabidopsis thaliana
                                                                 Herbicidal; plant; agriculture; herbicide.
                                                                                                                           Herbicidally active polypeptide SEQ ID NO 677.
                                                                                                                                                                                                                                                                                                                           ABB91466 standard; Protein; 598 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tietjen K. Weidler M:
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 Conservative

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Pred. No. 6.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 23; Length 573;
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RESULT 13
ABB63300
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                               brosophila melanogaster polypepti to SEQ ID NO 1602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB63300 standard; Protein; 762 AA
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N-PSDB; ABL07403
             WPT: 2001-656860/75
                                                Venter JC, Adams M,
                                                                              (PEKE ) PE CORP NY
                                                                                                               23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                27-SEP-2001.
                                                                                                                                                                                                                                 WC200171042-A2
                                                                                                                                                                                                                                                             Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                pharmaceutical.
                                                                                                                                                                                                                                                                                                              Drosophila, developmental blology well signalling insectibides
                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  ABB63300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; SEQ ID NO 677; 261pp + Semence Listing: English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tietjen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-AUG-1901; 1001WC-EP09892
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                                                                                                                                                            23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to identify ou target proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                598 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Weidler M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.3%,
85.7%;
                                                Li PWD,
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Pred No. 6.8e+02;
                                                Myors EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   multric acid or amino acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 23; Length 598;
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Query Match
Best Local Similarity
5: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                  insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                              specification, at ftp.wipo.in
                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 16692; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated restrict a id detection reagent for detecting 1800 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                          (ABB57737-ABB72072)
138 LKEYFT 143
                                                             1 IKEYFT 6
                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                762 AA:
                                                                                                                              Conservative
                                                                                                                                                                00 00
13 13 13
14 14
14 14
15 14 15
                                                                                                                              1: Mismatches
                                                                                                                                                          Score 30; DB 22;
Pred. No. 8.5e+02;
                                                                                                                           0: Indels
                                                                                                                                                                                        Length 762;
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SULT 14 B68116 ABB68116; ABB68116 standard; Protein: 833 AA

26-MAR-2002 (first entry)

Drosophila mėlanogastėr polypoptide SEQ ID NO 31140

pharmaceutical. Drosophila; developmental blology, cell signalling; insecticide

Drosophila melanogäster

WO206171042-A2

27-SEP-2001

23-MAR-2001; 2001Wc-US69231

23-MAR-2000; 2000US-191637P 11-JUL-2000; 2000US-0614150

(PEKE ) PE CORP NY

Venter JC, Adams M, Li PWD, Myers EW.

New isolate) modelic and deterribe reagent for detecting 1900 or more yenes from Drosophila and for elucidating cell signalling and cell-cell

Disclosure: SEO ID NO 31140: 21pp + Sequence Listing: English

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

diagnostic amino acid sequences of the invention

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RESULT 15
ABG15393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences (ABL01840-ABL16175) and the encoded proteins (ABB5777-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of murations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                               disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotid sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                  polypeptide (II) sequences. (1) is useful as hybridisation probes, polymerase chain reaction (PDE) primers, cligomers, and for chromosome and joine mapping and in recombinate production of (II). The polymelectides are also used in diagnostics as expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG15393 standard; Protein; 1028 AA
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               and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG00377 represent novel human
                                                                                                                     (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its buding partners are useful in medical imaging of sites expressing (II). (1) and (II) are useful for treating
                                                                                                                                                                                                                                                                                                             The invention relates to isolated (olynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID No 45752; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
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23-ANG-2000; 200008-6649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene ma;(ling; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-FEH-2002 (first entry)
                                                                                                                                                                                               for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (11) or to treat disease states involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US08631.
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85.7%;
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C Note: The sequence data for this patent did not appear in the printed c specification, but was obtained in electronic format directly from WIPO C at ftp.wipo in/published_pot_sequences.

X Sequence 1028 AA;

Query Match
Best Local Similarity 71.4%; Pred. No. 1.le+03;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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earch completed: April 8, 2003, 12:01:40
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# ALI :NMENTS

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Dest Local Similarity 100.0%, Score 25: DB 11, Length 54; Best Local Similarity 100.0%; Pred No. 33: Matches 5: Conservative 0: Mignatches 0: Indels
                                           Q63956;
Q63956;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last amoutation update)
                                    SEDUENTE
                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Cracinta, Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Soit anathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                  Fibrillin-1 (Fragment).
                                                                                                                                                                          Francke U.;
                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 NCBI_TaxID=10095;
                                                                                                                                                                                    Li X.,
                                                                                                                                                                                            MEDIINE-94140368; PubMod-8307578;
                                                                                                                                                                                                       TISSUE-LIVER;
                                                                                                                                                                                  Pereira L., Zhang H., Sangumeti C., Ramirez F., Bonadio J.,
                                     54 AA; 5747 MW;
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                                     KA4A AKABRKITZR TRO64;
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Query Match
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Monocyte chemoattractant protein-3 (MCP-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ251190; CAB61626.1; -.
HSSP; P13500; TDOK.
InterPro: IPPROPERIT: Chemokine_IL8
Pfam: PPO0049; IL8; 1.
SMART; SM00199; SCY: 1.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel 19 last annotation update)
Monocyte chemoattractant protein-2 precursor (Fragment).
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                                                                                                                            Asano K., Nakamura M., Oyuma T., Fukunaga K., Matsubara H., Ishizaka A., Yamaguchi K., Kanazawa M.;
"Differential expression of CC chemokines in guinea pig lungs during an allergic inflammation.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                  Cavia porcellus (Guinea pig).
Eukaryota: Metazoa. Chordata: Cramiata: Vertebrata: Euteleostomi:
         InterPro: IPR000827; CC_Shemkine_sml.
InterPro: IPR001811; Chemokine_ILB.
Pfam: PF00048; ILB; 1.
                                                                                EMBL; AB014340; BAA36456.1; -. HSSP; P51671; 1EOT.
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Mammalia: Eutheria, Rodentia, Hystricognathi; Cavildae:
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Vet. Immunol Immunopathol 76:283-298(2000).
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Mammalia: Eutheria; Perissodactyla; Equidae: Equus.
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SMART; SMOO199; SCY: 1.
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ilarity 100.0%;
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Best Local :
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                                                                                                                                                               Q9CWC7;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
2410150007Rik protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDI INE-2154447: PubMed-11677608: MEDI INE-2154447: PubMed-11677608: F. Thomson N.E. Fiskard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chil, Ingworth T., Connerton P., Cronin A., Davis P., Davies P.M., Isad L., White N., Farrar J., Cronin A., Davis P., Davies P.M., Isad L., White N., Farrar J., Cronin A., Davis P., Davies P.M., Isad L., White N., Farrar J., Cronin A., Larsen T.S., Leather S., Moule S., O'Goora P., Parry C., Guail M., Futherford K., Simmonds M., Skeiton J., Stevens K., Whitehead S., Barrell B.G.;
SEQUENCE FROM N.A.
SIPAIN=C578L/6J: TISSHE-EMBRYONIC SHEM CELLS:
MEDLINE-21085660: PubMed-11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M.,
Arakawa T., Hara A., Fukunishi Y., Kouno H., Ada
                                                                                                           Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciunognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of a multiple drug resistant Salmonella enterica serrovar Typhi (TTIA "; Nature 413:848-85/2001).
EMBL: AL513384; CAD09995.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last atnotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE: PS00472; SMALL_CYTOKINES_COSEQUENCE 97 AA; 11159 MW; E189Ai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CT18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella typhi.
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                                                                                            NCBI_TaxID-10090;
                                                                                                                                                            241015000781K.
                                                                                                                                                                                                                                                          29CWC7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=601;
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                                                                                                                                                                                                                                                                                                                                       63 LESYT 67
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nes 5; Conserv
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5: Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; ilarity 100.0%; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 25; DB
Pred. No. 67;
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82CA:3D5DB07760D CKC54;
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   Konno H., Adachi J., Fikuda
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 Itoh M., Ishii Y.,
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                                                                                                 Query Match
Best Local Similarity
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"The complete general fits streaming sufficient string P2."

Proc. Natl. Acad. Sci. U.S.A. 96:7835-7840(2001).

EMBL: AE006683: AA8470852.1;

InterProc. IRR002878: DUF35.

Pfam: PF01796: DUF35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-2132296: PubMed+11427726:
MEDLINE-2132296: PubMed+11427726:
She Q. Singh P. K. Confalonieri F., Zivanovic Y., Allard G.,
Awayez M.J. Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erause G., Flescher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng
Thi-Ngon H.P., Redder P., Schenk M.E., Therianit C., Tolstrup N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY 2000 (TrEMBLrel 13, Created)
01-MAY 2000 (TrEMBLrel 13, Last sequence update)
01-MAR-2000 (TrEMBLrel 20, Last annotation update)
Hypothetical protein $500532.
$500537 OP OFF-022_019
Sulfolobus solfatarious.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashizaki Y.; "Funotional annotation of a full-length mouse cDNA collection.": Nature 409:685-690(2001).
EMBL: AK019136: BAB3163.1; ".
MSD: MGI:1925497: 241015000781k.
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Salto T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sulfolobus.
                                                                                                                                                                                                                           Fram: Proless: 1.
ProDom: PD003834; DUF35; 1.
Hypothetical protein: Complete
SEQUENCE 133 AA: 14937 MW:
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Local Similarity 100.0%: Score 25; DB 11; Length 131;
Local Similarity 100.0%; Pred. No. 40;
hes 5; Conservative 0; Mismatches 2: 7:7:7
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56 LESYI 60
                                                     1 LESYT 5
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Okazaki Y. Gojoboli T. Bono H., Kasukawa I., Saito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cremarihaeuta, Thermiprotei, Sulfolobales, Sulfolobaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 AA;
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                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14901 MW; CBFFBFF76AC76AC4 CRC64;
                                                                                                                                        100.0%: Score 25; DB 17; Length 133; 100.0%: Pred. No. 91;
                                                                                                                                                                                                                              proteome.
7A6E83EECD3DA8E7 CRC64;
                                                                                                                Mismatches
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Saito R.,
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Best Local S
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Q95UR8;
Q1-pEC-2001 (TrEMBLrel. 19, Last sequence update)
Hyportherical 18 4 KDa protein
Macaca fascicularis (Crab eating merapha) (Cynomolgus monkay)
Macaca fascicularis (Crab eating merapha) (Cynomolgus monkay)
Eukaryota; Metazoa; Chadata, Cianina, Veriebrata, Eutheleostomi)
Mammalia; Eutheria, Primates; Catarnhini; Cercopithecidae;
Cercopithecidae, Macaca.
                                                                                                                                                                                               MEDITIRE-20083487, FubMed=10617197

Lin X., Kaul S., Rounsley S.D., Short T.P., Henito M.-I., Town C.D., Fujii C.Y., Mason T.M., Rowman C.I., Barnstead M.E., Feldblyum T.V., Roell C.F., Ketcham K.A., Leg T.T., Fonning C.M., Koc H., Moffat K.S., Cronin L.A., Shen M. Vanaken S.F., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Ocpenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.;

Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear class)
Eukaryota; Miridiplantae; Street Embryophyta; Tracheophyta;
Starmatephyta, Mannellephyta, Appl. Pyladins. Site Arabidots Field
eurosids II; Brassicales; Brassica wae: Arabidopsis.
NCBI_TaxID=4702:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NoV-1998 (TrEMBLrel, 08, Created)
01-NOV-1998 (TrEMBLrel, 08, Last sequence update)
91-MAB-2002 (TrEMBLrel, 20, Last and Latic, sphafe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     At2g26040 protein.
                                                                 S.E. T. A. (MAR-2000) to the EMRITED FAMILY OF PATHOGENESIS-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                080992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein. SEQUENCE 172 AA: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submithod (APG-2001) to the EMPL/Conkenk/DERT databases EMBL: AR070111; BAR63056.1; -.
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Interpro: IPPO00916; Bet_v_I.
pfam. pr00407; Bet_v_I; 1.
                                  EMBL; AC004747; AAC31232.1; -.
                                                                                                                            STRAIN-CV.
                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                 Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                          STPAIN-CV
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   266060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hashimoto K., Osada N., Rida M., Frenda J., Tanuma R., Hirai M.,
Terao K., Sugano S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                     PROTEIN.
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100.0%; Fred. No. 1.2c+02;
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Query Match
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Best Local .
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MEDLINE-2133296; FubMed-11427726;

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

De Moors A., Erauso G. Fletcher C., Gordon P.M.K.,

Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

The Complete genome of the crenarchaeon Sulfolobus scifataricus F2.":

Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q97220;
01-0CT-2001 (TrEMBLrel.
01-0CT-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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                                                                                                                                                                                                                                               01-JUN-1998 (TREMBEREL 06, Created)
01-JUN-1998 (TREMBEREL 06, Last sequence update)
01-MAR 2002 (TREMBEREL 20, Last annotation update)
Putative siama-B regulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE006676; AAK40756.1; --
InterPo; IPRO2C637: Ham.p_like.
Pfam; PF01725; Hamlp_like; 1.
ProDom: PD004952: Hamlp_like, 1.
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                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                              Bacillus lichemiformis.
Bacteria: Firmioutes: Bacillus/Clostridium group: Bacillales
                                                                                                                                                                                                                                                                                                                                                                          050233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGRFAMS; TIGR00042; Hamlp_like; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-2287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea: Crenarchaeota, Thermoprotei, Sulfolobales, Sulfolobaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sulfolobus solfatarious
Yand X., Kang C.M., Brody M.S., Price C.W.; "Opposing pairs of serine protein kinases and phosphatases transmit
                                              MEDLINE=96421969; PubMed=8824586
                                                                           STRAIN-FD50;
                                                                                                                                               NCBI_TaxID=1402;
                                                                                                                                                                            Bacillaceae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 LESYT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 LESYT 150
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hes 5: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LESYT 5
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                                                                                                                                                                            Bacillus.
                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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147 LESYT 151

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Query Match
Best Local Similarity
5, Conserve
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Thomas 5; Conserve
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Q8ZS45
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QBZ445;
QBZ445;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 21, Last simple update)
Q1-JUN-2002 (TrEMBLrel. 21, Last simotation update)
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SEQUENCE FROM N A
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MEDLINE=21595285; PubMed=11759840;

Kareko T., Makamura Y., Welk C.P., Kiritz T., Sasamoto S.,

Kareko T., Makamura Y., Welk C.P., Kiritz T., Sasamoto S.,

Watanabe A., Iriquchi M., Ishikawa A., Kawashima K., Kimura T.,

Watanabe A., Muraki A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00332; PP2Cc; 1.
SMART; SM00331; PP2C_SIG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene 212:111:118(1998).
EMBL: AF034567; AAC29511.1; -.
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                                                                                                                                                                                                                  DNA Res. 8:205-213(2001).
EMBL. AP003602; BAB77310.1; -
InterPro; IPP001982; Endonu-_LAG/HWH.
InterPro; IPR001005; MyD_DNA_Dind.H-1
FROSITE; PS00037; MYE_1; UNKNOWN__.
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Brody M.S., Price C.W.;
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                                                                                                                                                                 SEQUENCE
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Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid p007120beta
Bacteria: Cyamubacteria, Nostonal-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anabaena sp.
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                                                                                                                                                                                                 Plasmid:
                                                                                                                                                                                                                                                                                                                                                    cyanobacterium Anabaena sp. strain PCC 7120.":
                                                                                                                                                                                                                                                                                                                                                                                    Yasuda M., Tabata S.; "Complete genemic sequence of the illamentous nitrogen-fixing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=103690;
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     1 LESYT 5
                                                                                                                                                                    Hypothetical protein; Complete proteome.
216 AA; 25607 MW; A3F @D1@B1E555B3 CRC64.
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                                                            Conservative
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                                                                                                                   DB 16: Tength 216;
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Mationes
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EMBL; X77575; CAACAGE 2...
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01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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                                                                                                           MEDLINE-99310344: PubMed-10382866 H. Yamazaki S., Haikawa Kawaribayasi W. Hilo Y. Horikawa H., Yamazaki S., Haikawa Jin-no K. Takabashi M. Sekine M. Baba S.-T. Ankai A. Ko Hosoyama A. Enkui S. Nagai Y., Nishijima K. Nakazawa H. Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Ogrobi A. Aoki K.-T. Fubota K. Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
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        EMBL: AP000064: BAA81335.1; ...
InterPro: IPR004361; Glyckalase_1.
InterPro: IPR004360; Gly_bleo_diox.
Prfam: PF00903; Glyckalase: 1.
PROSETTE: PF00903; Glyckalase: 1.
                                                                                                                                                                                                                                                     Desulfurococcaceae: Aeropyrum.
NCBI_TaxID=56636:
                                                                                                                                                                                                                                                                                Aeropyrum pernix.
Archaea, Crematchaeota: Thermoprotei: Desulfutococcales:
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SMART: SMOO4/9: PHD: 1:
PROSTIE: PSO1186: ESE 2: HAKNOWN 1
SECURENCE 227 AA 25711 MU ECTARGEROA472E24 OFO64
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Bukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; Lilliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
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                                                                    orenarchaech, Aeropyrum pernix Ki.";
DNA Res. 6:83-101(1999).
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                           Hypothetical protein APE2519.
                                                                                                                                                                                                                                                                                                                                                                                     09Y8W5.
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PROSITE; PS00934; GLYOXALASE_I_1; UNKNOWN_1
                                                                                               "Complete genome sequence of an aerobic hyper-thermophilic
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                   235 AA
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01-MAY-1999 (TrEMBLrel, 10, Last sequence update)
01-JUN-2902 (TrEMBLrel, 21, Last sencitation update)
Hypothetical 25.6 kDa protein.
                STRAIN-GB-M1;
STRAIN-GB-M1;
MEDLINE-21576510; PubMed-11719806:
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01-JUN-2002 (TYEMBLIE)
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Pfam; PF00149; Metallophos; 1.
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EMBI: AF021091; AAD01686.1; the
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Enkaryeta: Merresperidia; Unikaryenidae: Encephalitezeon
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Jackson C.J., Pittman M.S., Clayton C.L., McColm A.A., Bagshaw J A.,
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Prensier G., Barbe V., Peyretaillade E., Brottler P., Wincker
                                                                                                                  STRAIN-GB-M1;
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Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
Weissenbach J., Vivares C.P.;
"Genome sequence and gene compaction of the eukaryote parasite
Encephalitzcon cuniculi.";
Nature 414:450-453(2001).
EMBL; AL590450: CAD26053:1: -.
SEQUENCE 262 AA; 29114 MW; CBACCA96EIDFD061 CPC64;
SEQUENCE 262 AA; 29114 MW; CBACCA96EIDFD061 CPC64;
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22 [OR Million cell updates/Sec
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### SUMMARIES

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# ALIGNMENTS

RESULT 2 Q9HJ/2 ID Q9HJ/2 AC Q9HJ/2; DT n1-MAP-2001	QY 1 IKEYETS	Query Match Sest Load Similarity Matches ', June			RT Expression RT monocytoge	"A"	ME:		OX NCBI_TAXID*1639;		CO Propression			AC 09ZIC6;	SU
PRELIMINARY: Tremblical: 16,	rs 7 !! rs 303	94 48; 85.78;	Hypothetical protein. SPOTENCE 548 AA: 62755 MW:	J. Bacteriol. 183:1133-1139(20 EMBL; AF033015; AAD01951.1; j.	Expression of Telchoic Acid-Associated Surtain monocytogenes of Serotype 4b.";	erotype-Specific Ge	MEDLINE=21101794; PubMed=11157924	30M N.A.	*1039;	Listeriaceae, Listeria	Partieria: Firmioutes: Barilli:	al 62.8 kDa protein. Chocytogenes	(TrembLrel. 10, (TrembLrel. 19,	(TrEMBLrel. 10,	PRELIMINARY:
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Lykke-Andersen J., Shu M.-D., Steltz J.A.;
"Human Upf proteins target an mRNA for nonsense-mediated decay when bound downstream of a termination codon.";
Cell 103:1121-1131(2000).
EMBL; AV013249; AAA0485991; -.
InterPro; IPR003890; IF_EIF4G.
Pram; PP02854; MIF4G; 3.
SMART; SM00543; MIF4G; 3.
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Mammalia; Eutheria; Primates; Catarrhini:
NCBI_TaxID=9606;
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EMBL; AF301013; AAG63625.1; -.
EMBL; AF318574; AAG66689.1; -.
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Mendell J.T., Medghalchi S.M., Lake P.G., Noensie E.N., Dietz H.G.;
Mendell J.T., Medghalchi S.M., Lake P.G., Noensie E.N., Dietz H.G.;
Novel Upf2p Orthologues Suggest a Functional Link between Translation
Initiation and Nonsense Surveillance Complexes.";
Mol Cell Biol 20:8944-8957(2000)
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Rukarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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elegans SMG-4);";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15,
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Fred. No. 1.7e+02,
1, Mismatches 0; Indeis
                                                                                                                                                                 Score 34; CB 4;
Pred. No. 1.7e+02;
1, Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                      95F3C57D2854BB44 CEC64;
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RESULT 4
Q9F2D9
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Best Local Similarity
6 Conserv
Query Match
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Matches 6; Conserv
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 27.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09P2D9;
01-0CT-2000 (TrEMBLrel 15, Created)
01-0CT-2000 (TrEMBLrel 15, Last sequence update)
01-JUN-2002 (TrEMBLrel, 21, Last amoutation update)
                                                                                                                                                      Yu J., Wang L., Ho X., Pang Y.; Submitted (pb:-1200) to the EMBL(Th::Bulk,TDBJ databases EMBL) AF325155; AAL01783.1; -. Hypothetical protein.

SEQUENCE 236 AA. 27163 MW: F83198C717FA8F05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003890; IF_eIF4G. Pfam; PF02854; MIF4G; 3. SMART; SM00543; MIF4G; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KIAA1408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleopolyhedrovirus Genome.";
Virology 287:391-404(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spodoptera litura nucleopolyhedrovirus.
Viruses; dsDNA viruses, no RNA stagn; Baculoviridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                091BC8
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The complete sequences of 150 new CDNA clones from brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                   STRAIN=G2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pang Y., Yu J., Wang L., Hu X., Bac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21425398; PubMed=11531416;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence Analysis of the Spondopter olivera Multicapsid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         382 LKEYFTS 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   υı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IKEYFTS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Res.
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        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=10718198;
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85.78;
        100.0%; F
                                         88.9%; Score 32;
100.0%; Pred No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150653 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ishikawa K., Hirosawa M., Ohara O.;
ding sequences of unidentified human genes.XVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score (4: DB 4; Pred. No. 1.7e+02; 1: Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT
        Mismatches
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                                                                               Length 236;
            Indels
        0;
            Gaps
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91 KEYETS 96

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x MEDLINE 9928-316; FubMod=10360571;
A Nelson K E. Clayton P A., Gili S P., Gwinn M.L., Dodson F.J.,
A Haft D.H., Hickey E K., Peterson J D., Nelson W C., Ketchum K.A.,
A McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
A Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
A Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
A Selzberg J.J., Sunth H.O., Vencer J.C., Fraser C.M.,
"Evidence for lateral gene transfer between Archaea and Bacteria from Greenome sequence of Thermotoga maritima.";
A Nature 39:123-339(1999).
A Nature 39:23-339(1999).
B HSSP, 005701; AAD35134.1; -.
B HSSP, 005701; AAD35134.1; -.
B FIGTERPO: IPP000409; Dhdrppt_synt.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Wilson R., Ainscoudh E., Anderson K., Baynes C., Berks M., Ronfield T. Burton T. Connell M. Copsey T. Cooper J. Coulson A. Craxton M. Dear S. Du Z. Burbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Jones M., Kershaw J., Kirsten J., Laister N., Colliaghan M., Parcy G., Rifken L., Morthore B., O'Callaghan M., Smaldon M. Smith A. Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
                                                                                                                                                                                                                                                                                                                                        01-JUN-1998 (TrEMBLrel, 06, 01-JUN-1998 (TrEMBLrel, 06, 01-DEC-2001 (TrEMBLrel, 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel 12, Created)
01-NOV-1999 (TrEMBLrel 12, Cast segretore opdate)
01-JUN-2002 (TrEMBLrel 21, Last annotation update)
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                                                                                                                                                                STRAIN-BRISTOL N2: MEDLINE-94150718: PubMed-7906398;
                                                                                                                                                                                                                                                     Rhabditidae: Peloderinae: Caenorhabditis
                                                                                                                                                                                                                                                                                        Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                         K∩4H9 5 protein
                                                                                                                                                                                                                                                                                                                                                                                                                044990
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                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                               044990:
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                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.9%, Score 32, 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                            Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                           Created)
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le+02;
hes 0; Indels
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RESULT 9
Q972GR
ID Q972
AC Q972
DT 01.D
DT 01.H
DE Hypo
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Best Local :
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097208 FRELIALMANA,
097208;
01-7520-2001 (TrEMBLERI, 19, Created)
01-DEC-2001 (TrEMBLERI, 19, Last requence update)
01-MAR-2002 (TrEMBLERI, 20, Last repetition update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Madsen C., Graves T., Blair T.;
"The sequence of C. elegans cosmid KU9H9.";
Schootted (IAN-1199) to the EMBL, **PREKECEPT databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-96213687; PubMed-8647250; Schlenzka W., Shaw L., Kelm S., Schuldt C.L., Bill F Schlenzka W., Schauer R.; Cottspeich F., Schauer R.; "CMP-M-acetylneuraminic acid hydr wylaso The first iron-sulphur protein to be described in Eurykarya."; FEBS Lett. 385:197-200(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fikaryota: Metazoa: Chordata: Craciata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Cetartiodactyla: Suina: Suidae: Sus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Watson A., Weinstock I., Wilkinson Sproat T., Wohldman P.:
"2.2 Mb of configuras moderable repercer from chromosome III of
elegans.";
                                                                                                                                                                                                                                                                                                                          SEQUENCE 435 AA: 50528 MW: 568416306829080 CRC64:
                                                                                                                                                                                                                                                                                                                                          Monotoxygenase, Oxidoreductase, NON_TER 1 1
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                                                                                                                                                                                                                                                                                                                                                                         EMBL; Y15010; CAA75243.1;
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                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-1997) to the FMRL/SunBack/DDBT databases
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                                                                                                                                                                                        316 IKEYFT 321
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6; Conserv
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100 0%; Pred No 1 5e+02;
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SULT 11
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Best Local
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Kawarabayasi Y. Hino Y. Horikawa H. Tiu-no K. Takahashi M. Kawarabayasi Y. Baba S.-I. Ankai A. Kosugi H. Hosoyama A. Fukui S., Sekine M. Baba S.-I. Ankai A. Kosugi H. Hosoyama A. Fukui S., Nagai Y. Nishijima K. Otsuka R. Nakazawa H. Takamiya M. Kato Y., Nagai Y. Tanaka T. Kudoh Y. Yamazaki J. Kushida N. Guchi A. Yoshitawa T., Masuda S., Yanagii M. Nishimura M. Yamagishi A., Oshima T. Kikuchi H.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9Y471;
01-NOV-1999 (TrEMBLrel: 12,
01-NOV-1999 (TrEMBLrel: 12,
01-NOV-1999 (TrEMBLrel: 12,
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Hypothetical protein: Complete proteome.

SEQUENCE 479 AA; 54377 MW; 5C76E4E7151B5332 CRC64:
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Sulfolobus tokodaii
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
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                 O9BTR8:
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Cytidine monophosphate-N-acetylnouraminic acid hydroxylase
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J. Biol. Chem. 273:15866-
EMBL: D86324; BAA31160.1;
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(CMP-N-acetylneuraminate monooxygenase).
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hes 6: Conservative
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nes 6; Conserv
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AP000985: BAB66241.1: -.
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09WV23;
01-NOV-1999 (TrEMBLrel. 12, C
01-NOV-1999 (TrEMBLrel. 12, L
01-DEC-2001 (TrEMBLrel. 19, L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stauffer R.L., Walker A., Ryder "Human and ape molecular clocks hypotheses.";
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01-MAR-2002 (TEMMBLER) 20, Last sempence update)
01-UNN-2002 (TEMMBLER) 21, Last annotation update)
CMP-N-acetylneuraminic acid hydroxylase (Fragment).
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Rukaryota, Metazoa, Chordata: @rani::: Vertebrata: Euteleostomi:
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                                                                                                                                                                                            Cricetulus griseus (Chinese hamste:).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Rodentia: Sciuroquathi: Muridae: Cricetinae:
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"cDNA sequence of CHO cnah.";
Submitted (JUN-1999) to the bMbL/coumanh/EdRI databases.
                                                                                                                                       NCBI_TaxID-10029;
                                                                                                                                                                        Cricetulus.
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                                                           Goergen J.L., Chenu
                                                                                     SEQUENCE FROM N.A
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497 AA,
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100.0%; Pred. No. 1.8e+(
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100.0%; Pred. No. 1.8e+02
+1v== 0: Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                          Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                             PRT:
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and constraints on paleontological
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-61419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q91UJ2;
Q9TUJ2;
SEQUENCE FROM N.A.
ITHE A., SHZUKİ A.;
"Molecular evolution of CMP-NeuAc hydoxylase in primates.";
Submitted (MAY-1998) to the EMBL/AD-HEARK/FDRJ databases.
EMBL; AB013814; BAA86057.1; -.
InterPro; IPR001281; Rieske.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-BALBYC: TISSUE-LIVER:
MEDLINE-95332362; PubMed-7608218;
MEDLINE-95332362; PubMed-7608218;
Kawano T., Koyama S., Takematsu H., Kozutsumi Y., Kawasaki H.,
Kawashima S., Kawasaki T., Suzuki A.,
Molecular cloning of cytidine monophospho-N-acetylneuruminic acid
"Molecular cloning of cytidine monophospho-N-acetylneuruminic acid
hydroxylase.";
"J. Biol. Chem. 270:16458-15463(1995).
EMBL; D21826; BAA04850.1; *.
MGD; MGI:103227; Cmah.
MGD; MGI:103227; Cmah.
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Q61419;
                                                                                                                                                                                                                                                                                       01-MAY 2000 (TrEMBLrel 13, Created)
01-MAY 2000 (TrEMBLrel 13, Last sequence update)
01-DEC 2000 (TrEMBLrel 19, Last annotation update)
01-DEC 2001 (TrEMBLrel 19, Last annotation update)
CMP-N-acetylneuraminic acid hydroxylase.
Macaca mulatta (Rhesus macaque).
Eukaryota: Matazoa: Chordata: Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro: IFR001281; Rieske,
Ptam: PF00155; Rieske; 1.
SEQUENCE 577 AA; 65945 MW; 6808ECC75E4F6B78 CRC64;
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NON_TER 1
NON_TER 563 563
                                                                                                                                                                                                                                NCBI_TaxID-9544;
                                                                                                                                                                                                                                                                  Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota: Metazoa: Chordata: Craniata; Vertebrata: Euteleostomi;
Mammalia; Eutheria: Rodentia: Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-N-V-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      458 IKEYFT 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       454 IKEYFT 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         563 AA, 65105 MW; F62726BA5429359D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.4%: Score 32; DB 11; Length 577; 100.0%: Pred. No. 2.1e+02;
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    Mismatches

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                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
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DR Pfam; PF00355; Rieske; 1.

SQ SEQUENCE 590 AA; 68256 MW; 32104474A2908A95 CRC64;

Query Match
Bost Local Similarity 100 6%; Prol No. 2.1e+02;
Matches 6, Conservative 0; Mismatches 0; Indels 0; Gaps

Oy 1 IKEYFT 6

[11]
Db 458 IKEYFT 463
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Search completed: April 8, 2003, 12:04 17 Job time: 68.4167 secs